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                                                             32300 SEA FILE=FEGISTEY APR:01 Light Light
            1510) SEA FILE=FEGISTRY FAM: 1532(4-43--,) ABB=ON 14 OR L4 17000 SEA FILE=FEGISTRY AFB:ON 14 NOT 16
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L.G
                % SEA FILE=HUAFLU: ABB=DN | 116 AUD DELTA(W (15 DE 12)
10 SEA FILE=HUAFLU: ABB=DN | 116 AUD MUTANT?
30 SEA FILE=HUAFLU: ABB=DN | 115 AUD MUTANT?
L17
Lit
L.. l
                FILE=HUAPLUM ABB=UN III AUD UMTANTA
L. 3
                 4 SEA FILE=HUAPLUU ABBEUN 121 AND DELTA(W (12 OR 15)
La. 5
                19 SEA FILE=HUAPLUS ABB=UN 118 JR L22 OR L23
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= d 124 1-19 white abs ind
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L24 ANSWER 1 OF 19 HCAPLUS CUPYRIGHT 1997 ATS KATHLEEN FULLER, BT, LIBRARY 308-4290

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1997:628484
             - Document No. 127:316834 Rapid and transient induction of a
     parshey microsomal .DELTA.12 fatty
     acid desaturase mRNA by fungal elimitor. Hirach,
     Christoph; Hahlbrook, Klaus; Somssich, Imre E. (Max-Planck-Institut
     fur Stathtungsforschung, Abteilung Bioch-mie, Cologne, D-50829,
     Germany). Plant Physich., 115(1), 283-130 (English) 1907. CODEN:
     FLPHAY. 188N: 0031-0889. Publisher: American Society of Plant
     Physiplogists.
     Treatment of cultured parsley (Fetroselinum brispum) cells with a
AB
     structurally defined paptide elicitor (Pap25) of fungal brigin has
    providually been shown to cause rapid and large changes in the levels
     of various desatd. fatty acids. Two
    distinct parsley ofMAs were isolated sharing high sequence
     simularity with microstmal .omega.-6 fatty acid
     desaturases (FADs). One of them was functionally identified
     as a .DELTA.12 FAD by empression in the yeast
     Sandrianomydes derevisiae. Two dientic fatty adids, hexadebadientic
     and linoleic, which were not detectable in control cells, together
     constituted up to 1. Of the total fatty acids in the transformed
     yeast bells. .DELTA.12 FAD mRNA abbumulated
     rapidly and transiently in elicitor-treated parsley cells,
     protoplasts, and leaves. These and previous results indicate that
     fatty acid desath. Is an important early
     component of the conglex defense response of parsley to attempted
     fungal infection.
CC
     11-L (Flant Biconemistry)
    Section grass-reference(s): 3, 7
     paraley fatty acid desaturase fungal
     elimiter; infection fungi parsley fatty acid
     desaturase; Pepil olicitor fatty acid
     desaturase paraley
     Ebytialexin-eliditing hormones
     FL: PAC (Biological activity or effector, except adverse); BIOL
     (Barological study)
        (Rep 20; rapid and transient induction of a parsley microsomal
      .DELTA.12 fatty acid
      desaturase mENA by fungal elicitor)
    cDML sequences
        (for paraley microschal .DELTA.12
      fatty acid desaturase responsive to
        tungal edicitor,
     Protein seguences
        fuf paraley microscorel .DELTA.12
      fatty acid desaturase responsive to
        rungal eligitor
ΙT
     Earnley (Retroselinum orispum)
        Trapid and transient induction of a parsley microsomal
      .DELTA.12 fatty acid
      desaturase mRNA by fungal elicitor)
     197594-14-2 197594-15-3
ΙT
     FL: FPM (Biological process); PRP (Proporties ; BIOL (Biological
     atudy:; PROC (Epodera)
        commind acid sequence; rapid and transient induction of a parsley
        miprosemal .DELTA.12 fatty
     acid desaturase mEMA by fungal elicitor)
18.442-90-4, GenBank U75743 187698-97-3
ΙT
     FL: BPH (Piclogical process); PEP (Properties); BIOL (Biclogical
     study); PROC (Process)
        indulectide sequence; rapid and transient induction of a parsley
        ralcrosomal .DELTA.12 fatty
      acid desaturase mENA ky fungal elicitor)
     \tilde{c}46J\vartheta-41-9, Fatty acid .DELTA.
     12-desaturase
     KL: BPE (Biological process); PEP (Properties); BIOL (Biological
```

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study); PROC (Process)
        (rapid and transient induction of a parsley microsomal
      .DELTA.12 fatty acid
      desaturase mPMA by fungal elicitor)
ΙT
     67826-35-4, Fatty acid .omega.-3
     desaturase
     EL: BST (Biblogical Atudy, unclassified); PRP (Properties); BIOL
     (Biological study)
        trapid and transient induction of a passley misrosomal
      .DELTA.12 fatty acid
      desaturase mEMA by fungal elicitor:
L24 ANSWER 2 OF 19 HOAPLUS COPYRIGHT 1997 ACS
             Document No. 127:25944: The pleate desaturase product of
1997:010711
     the FALC-N genu of hazel and its uses. Dani, Maria; Catello, Sergio
     (Spremartoe S.A., Belg.; Ferrero S.P.A.). Eur. Pat. Appl. EP 794250
     A1 970910, 29 pp. DESIGNATED STATES: E: BE, ES, FR, GB, IT, NL. English). CODEN: EPXXOW. APPLICATION: EP 97-103098 970226.
     FRIORITY: CH 9.-550 960804.
AΒ
     The FADD-N gene of hazel (Corylus swellang L.) coding for the .
     DELTA.12 desaturuse enzyme of the microsomal
     fraction is bloned and characterized for use as a probe for the
     is plation of other plant desaturase genes. The gene can also be
     used to alter the desaturase levels and consequently the
     fatty-acid compn. of a plant. Propes derived from
     the Arabidopsis .DELTA.12 desaturase gene were
     used to sureer a nazel cDNA benk from ripo Corylus avellana ov. San
     @ipwanni in .lambda.JAPII.
     10M | DILN 15-5:
10D | DILN015-6D; C12N609-02; C12N606-10; C12Q301-66
TC
ICA ACCHOS-00
CC
     Tel (Encymes)
     Seption pross-reference(s): 7, 11, 17
ST
     deltal/ desaturase gone PAD2M Corytus; hadel deltal/ desaturase gene
     FAD: N
ΙT
     Genes (plant)
     HL: PSU (Biological study, unclassified); PRE (Properties); BICL
     (Birlagroul study)
        .PAC.-U; cleare desaturase product of PAD2-N gene of hazel and
        ita waka)
ΙT
     INA sequerices
     cDNA seguences
        'fir .DELTA.12 desaturase of hazel; oleate
        desaturase product of PAD. -N dene of hazel and its uses
     Fate and Hyperidic oils, biclogical studies
     8L: AGA, (Agricultural use); BOC (Ficlogical cocurrence); FFD (Food
     or feed user; BIOL (Biological study); OCCU (@dourrence); USES
     т Эве в Т
        That limit, elemina of desaturase gene for altering
      fatty acid profile of; oleane
      desaturase product of FADR-N gene of hazel and its uses)
ΙT
     Fatty smids, biological studies
     RL: AGR (Agricultural use); BOC (Biological occurrence); FFO (Food
     or feed user; BIOL (Biblogical study); 0000 (Occurrence); USBS
         of hazel, of ming of desiturase gene for altering profile of;
        colleane desaturase product of PADS-N gene of hazel and its uses)
TI
     Protein sequence:
         cf .DELTA.12 desaturase of hazel; bleate
         tesaturase product of FADN-M gene of hazel and its uses;
ΤТ
     Hazel (Corylus avellana)
         cleate desaturase product of FAD2-N gene of hazel and its uses)
IT
     Endoplasmic reticulum
         (.DELTA.12 desaturase of nazelnut; oleate
                            KATHLEEN FULLER BT/LIBRARY 308-4290
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```
desaturase product of FADS-N some of hazel and its uses)
ΙT
       196217-78-4
       EL: AGR (Agricultural use); ESU (Biological Study, unclassified);
       PRP (Properties); BIOL (Buol gloal study); USES (Uses)
           (amino abid sequence; deste desaturase product of FAD. -N gene of
           hadel and its uses)
ΙT
       196217-80-8
       EL: BCT (Biological study, unclassified); PRP (Properties ; BIOL
       (Biological study)
           (amin: adid sequence; oleate desaturase product of FALC-N gene of
           hasel and its uses)
       1 1621 := 17 = 3
                          19-217-79-8
                                            19631 - 11-3
ΙT
       EL: ASS. (Agricultural use ; BSU (Biological study, unplessified);
       ETU (Biological use, unclissified); PAP (Properties); Blot (Biological study); USES (Uses)
           (mucleotine sequence; pleate desaturate product of FAD. -N gene of
           nadel and its uses)
       59929-36-1, Oleane desaturase
ΙT
       FD: BSU (Biological study, unclassified); PEP (Properties); BIOL
       (Biological study)
           (bleate desaturase product of FADS-H gene of hazel and its uses)
                                                                                               par elenie
L24 ANSWER 3 OF 19 HOAPLUS CORVEIGHT 1997 ACS 1997:813089 Topument Mo. 127:15 394 Plants having mutant
       sequences that confer altered fatty acid
      profiles. | DeBonte, R. Lirin; Ban, Theyong; Lon, H.-T. Willie (Cargill, Theorperated, USA; DeBonte, E. Lorin; Fan, Theorong; Loh,
      H.-T. Willier. FCT Int. Appl. WO 9721-40 At 470619, 67 pp. 
IECICUATED STATES: W: AL, AM, AT, AS, AS, BB, BG, BE, BY, CA, CH,
      TECHOLATED STATES: W: AL, AH, AT, AC, AH, BD, BO, BC, BC, CA, CH, CD, CD, DE, DM, EE, ES, EI, GE, SE, HU, DL, TC, CP, ME, PG, MP, MR, MU, LE, LE, LA, ET, LU, LU, MD, MG, MM, HM, MW, MK, MO, MC, PL, PT, EG, FT, SD, SE, DG, SI, SE, TC, TM, TE, TT, UA, UG, UG, UI, VN, AM, AD, BY, MG, ME, MD, EU, TJ, TM; EM; AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, EA, FT, FR, GA, GB, GE, TE, LT, LU, MC, ML, ME, NE, NL, PT, SE, SN, TD, TG. (English). (CODEN: PIKKD: APPLICATION: WO SHOW ISSET THE STATES OF STATES OF STATES OF STATES OF STATES.
      Sweds, plants and oils are provided having low FDA sats., high oleic
      a md, low lintlels adid,; high or low pauritic acid, low stearid
      actio, and low fineleic and plus linelenge actd, and admintageous functional or nutritional properties. Plants are disclosed that
       centain a mutation in a delta-12 or
       delta-15 fatty acid
      desaturase gene. Preferred plants are rapeseed and sunflower plants. Flants carrying such mutant genes have
      alter a fatty acid compon. in seeds. In one
      erBodiment, a plant contains a mutation in a region having the conserved motif His-Kaa-Kaa-Hiz, found in delta-
       12 and delta-15 fatty
       acid desaturases. A preferred motif has the
       sequence His-Glu-Cys-Gly-His. A preferred mutation in
       thus motif has the amino acid sequence Hase-Lyn-Cys-Gly-His. Nucleic
       avad transents are discloved that comprise a mutant
       delta-12 or delta-15
       fatty acid desaturase denn sequence.
IC
       ICM A[1H]:[1-16
            A01H005-10; A01H001-00; C12N015-00; C07C057-02; C07C057+03;
       [+15
             0070353-126
CC
       1 -9 Fice and Food Chemistry)
       Sobti n pross-reterence(s): 11
ST
       fatty acid profile alteration plant
       mutation; brassina fatty acid profile
       alteration mutation; Helianthus fatty
       acid profile alteration mutation
ΤT
       Pollination
```

```
(cross; plants having mutant sequences that confor
        altered fatty acid profiles)
ΙΤ
     Genes
     PL: BAC (Biological activity or effector, except adverse); BIOL
     (Biological shudy)
        (microsoma); plants having mutant sequences that confer
        altered fatty acid profiles;
ΙT
     Brassida dampestria
     Frassida napud
     Cruciferae (Brassicaceae)
     Helianthus
     Mutagenesis
    Mutation
        (plants having mutant sequences that confer altered
      fatty acid profiles)
     Fatty acids, liplogical studies
ΙT
     FD: BOC (Bitlegical occurrence); BPE (Biological process); BIOL
     (biological study); 0000 (Opourrence); PROC (Process)
        (plants having mutant sequences that sinfer altered
      fatty acid profiles)
ΙT
     Trigetable oils
     EL: FOC (Biclogical comurbence); EEM (Removal or disposal); BIOL
     Swiclegical study); 0000 (Openmender; PBed (Process)
        (plants having mutant sequences that dinfer altered
      fatty acid profile?)
TΨ
    Cancla oil
     FL: BPR (Piplogipal process); BIOL (Biological study); PROC
     (Process)
        (plants having mutant sequences that confer altered
      fatty acid prifiles)
     el=80=0, Ethylmethanesulfonate
                                       71427-04-3, .DELTA.
TΤ
     15-Fatty acid desaturase
     01536-70-0, .DELTA.12-Fatty
     acid desaturase 192891-61-
                                       190691-62-6
     1.00891-63-7 191891-64-8
     FM: PAC (Biological activity or effector, except adverse); BIOL
     :Bloubgical Study:
        (plants having mutant sequences that denfer altered
      fatty acid profiles)
     142889-74-0 192889-75-1 102889-79-5
                               19. #83-74-2 192889-77-3
TT
                               190883-50-5 192889-81-9
     FM: BAC (Biological activity or effector, except adverse); BPR
     (Budlogical pictoss); #IOW (Biological study); EROC (Process)
        (plants having mutant sequences that dinfer slitched
     fatty acid profiles)
ΙT
     *T-10-3, falmitic acid, biclomical studies - 37-11-4, Stearic acid,
     biological studies (60-83-8, Lincieid adid, biological studies
     110-80-1, Oleic acid, biolog. al studies -463-40-1,
     .alpha.-Binclenic acid
                                1928/3-84-4 19 323-59-5
     19.3623-57-7 19.323-53-53-5
     FL: BOC (Biog. dical obcurrence); F101 (Bi dogical study); OCCU
     Maidurner. de L
        (plants having mutant sequences that confer altered
      fatty acid profiles)
L24 ALUMER 4 OF 1: HCAPLUS COPYRIGHT 1:97 A43
1997: Plass | Coroment No. 126:289:96 | Microbial and plant genes for
     .DEDTA.6-deseturases and their use in increasing tibsue levels of
     .pamma.-limelenic acid. Thomas, Terry L.; Ready, Aratu S.; Nuccio,
     Michael; Numberg, Andrew N., Freyssinet, Georges L. (Shone-Poulond
     Approximie, Fr.). U.S. US 5614391 A 970325, 30 pp. Cont.-in-part
     of U.S. 5,552,506. (English). TODEN: USKKAM. APPLICATION: US 34-566779 941230. PRIORITY: US 31-704475 311010; US 92-817919 320168; US 98-353952 921013; US 94-307382 940914.
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AB
    Microbial genes for .DELTA.6-desaturases are sloned and
     characterized for use in the prepn. of transgenic organisms
     synthesining high levels of .pamma.-linelenic acid from lineleic
     abid. Plants expressing a desaturase gene and with high tissue
     levels of .gamma.-linclenic acid are chilling resistant. These
     plants can also be used to produce bils with altered levels
     .gamma.-Linblenic acid. The Symechicystis .DELTA.6-desaturase was
     clone: by expression in a .gamma.-linolenate-deficient Anabena.
     Expression of the gene in transgenic tobacco and carrot is
     demonstrated.
    ICM 120015-55
IC
          1121018-82; C12N001-21; C109007-64
NCL
    435134000
CC
     7-1 (Enzymes)
ST
     delta: desaturase gene Synechicystis borage; gamma linolenate manuf
     deltar desaturase
     Plasmad vectors
TT
        (1..1.1.1)ELTA.6NOS, borage .DELTA.6-desaturase gene on, expression
        in pairest dell culture and tobacco of; microbial and plant genes
        for .DEDTA.6-desaturases and their use in increasing tissue
        levels of .gamma.-linosenic acid:
     Plasmid vectors
TΤ
        (2.1..DELTA.6NOS, borage .DELTA.6-desaturase gene on, expression
        in carret deal dulture and tobacco of; microbial and plant genes
        fi: .UELTA.6-desaturases and their use in increasing tissue
        levels of .gamma.-line.enic acide
TT
    -Garret
        (coll cultures as expression host; microbial and plant genes for
        .DELTA.6-desaturases and their use in increasing tissue levels of
       .famma.-linclenic acid:
ΙT
     Coare
     Bilamentous fungi
     Pearest.
     Fape (plant)
     Soywean
    Sünflewer
     Lobació
        (expression host; microbial and plant genes for
        .DFLTA.6-desaturases and their use in increasing tissue levels of
        .damma.-linclenic acid
    Anabacha
ΙT
        (empression of .DELTA.6-desaturase genes from carboxylase
       primoter of; microbial and plant genes for .DELTA.6-desaturases
        and their use in increasing tissue levels of .gamma.-linolenic
       acted)
    Glyminins
ΙT
     RL: MSC (Miscellaneous)
        rempression of .DELTA.6-desaturase genes from promoter of gene
        for; microbial and plant genes for .DELTA.6-desaturases and their
       use in increasing tissue levels of .gamma.-linolenic acid)
ΙT
     350 promotor (penetic element)
     EL: B''l 'Biblogical use, unclassified); BIOL (Biological study);
     SES 23. 31
         empression of .OELTA.6-desaturase genes from; microbial and
        plant genes for .DELTA.6-desaturases and their use in increasing
        tiusur levels of .gamma.-linolenia acid)
     DMA siguinales
         for .DBLTA.6-desaturase of Synechocystis; microbial and plant
        quies for .DELTA.6-desaturases and their use in increasing tissue
        levelt of .gamma.-linolenic acid)
ΙT
     cDNA sequences
        for .DELTA.6-desaturase of borage; mitrobial and plant genes for
        .DELTA.6-desaturases and their use in increasing tissue levels of
        .gamma.-linolenic acid;
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ΙΤ
     Genes (microbial)
     Genes (plant)
     PL: BUU (Biological use, unclassified); PRP (Properties); BIOL
     (Bitlogical study); USES (Uses)
        ofor .DEDTA.6-desaturase, cloning and expression of; microbial
        and plant genes for .DELTA.6-desaturases and their use in
        increasing tissue levels of .gamma.-linolenic acide
     Olobulins, miscellaneous
ΙT
     BL: MSC | Hisbellanebas)
        chelianthinins, expression of .DELFA.6-desaturase genes from
        promoter of gene for; microbial and plant genes for
        .DELTA. 6-desaturases and their use in .noreasing tissue levels of
        .gamma.-linolenio acid)
    Globulins, miscellaneous
     FL: MSC (Misbellaneous)
        (meliar.thins, expression of .DELTA.6-dusaturase genes from
        promoter of wene for; miorobial and plant genes for
        .(ADTA.6-desaturases and their use in increasing tissue levels of
        . (amma.-linolenic abid)
ΙT
     Erometer (denetid element)
     FL: FUU 'Biological ase, unclassified); BUOL (Biological study);
     USES (Uses)
        (nemologous and neterologous, expression of .DELTA.6-desaturase
        dones from; midrobial and plant genes for .DELTA.6-desaturases
        and their use in intreasing tissue levels of .damma.-linologic
        5 (i i)
ΙT
     Albumins, miscellanecus
     FL: MSC (Misbellaneous)
        quapins, expression of .OELMA.8-desaturase genes from promoter of
        gone for; midrobial and plant genes for .DEDTA.6-desaturases and
        their use in increasing tissue levels of .gamma.-linclenic acid)
     Erst in sequences
ΙT
        of .IWLTA. 6-desaturases of Symeonocystis and borage; microbial
        and plant genes for .DELTA.6-desaturases and their use in
        increasing tissue levels of .gamma.-linolenic abid:
ΙT
    Cold stress (plant)
        Cransgenic plants resistant to; miorbhial and plant genes for
        .!ELTA.6-desaturases and their use in increasing tissue levels of
        . mamma.-linolenio adid
     Borage officinalis
IT
     Zyne modystis
        r.SELIA.6-desaturase gene of; microbial and plant genes for
        .TEDTA.6-desaturases and their use in increasing tissue levels of
        . pamma.-linclenic acid:
ΙΤ
     148734-39-8 180583-92-0, Desaturase, linoleate
     (Borago difirinalis)
     FL: AGR -Agricultural use:; BSU (Biological study, unclassified);
     FRP (Frogerties); BIOL (Biological study); USES (Uses)
        (amino acid sequence; microbial and plant genes for
        .1BLTA.6-desaturases and their use in increasing tissue levels of
        .:amma.-linolenic acia:
     9051-35-4, Carboxylase
IΤ
     PL: MSC (Miscellahecus)
        (expression of .DELTA.6-desaturase genes from Anabona promoter of
        gene for; microbial and plant genes for .DELTA.6-desaturases and
        their use in increasing tissue levels of .gamma.-linclenic acid)
     7142 -04--9, .DELTA.15-Desaturase
ΤT
     8462 - 21- 3P
     FL: ADR (Adricultural Use); BPN (Bibsynthetic proparation); FAP
     (Properties); BIOL (Biological study); PREP (Preparation); USES
     (Used)
        (gene for, in engintering fatty acid
        profiles; microbial and plant genes for .DELTA.6-desaturases and
        their use in increasing tissue levels →f .qamma.-lin>lenic acid)
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ΙΤ
     °1275-16-9P, octadecatetraenoic acid
     F.L.: BFM (Bibsynthetic preparation); FROL Biological study); FREP
     (Preparation)
         (manuf. with transgenic microorganisms, .DELTA.\epsilon-desaturase genes
         in; microbial and plant genes for .DELTA.\ell-desaturases and their
     use in increasing tissue levels : .qarma.-linolen:: scid) #082-66-0P, .DBLTA.6-Desaturasq
ΙT
     FL: AGE (Agricultural use); BFN (Bicsynthetic preparation); PEP
      Properties); BIOL (Billogical study); PEEP (Preparation); USES
      Hace:
         unicrobial and plant genes for .DRIMA. \theta -desaturases and their use in increasing tissue levels of .panma. -limblenic asid:
     463-46-1, . . . . . Linclenic acta
ΙΤ
     FB: FBY (Biological study, Unclassified); BIQS (Biological study)
         .m.crotrganisms producing, manuf. of .gamma.-linolenate with;
        microbial and plant genes for .DELTA. \epsilon -desaturases and their use
         in increasing tissue levels of .gamma.-linelenic acid)
     1:00 88-98-8 190888-91-9 190088-60-0
ΙΤ
     BB: AGE (Agricultural use); BBU (Bibliogical study, unclassified);
     FRP (Freperties : BIOL (Biological study : USES (Uses.
         (nucleatide sequence; midrobial and plant genes for
         .DELTA.6-desaturases and their use in increasing tissue levels of
         .gamma.-linolemin acid)
     108-26-38, .gamma.-Linelenco abid
ΤT
     Fh: AGE (Agricultural use); SPU (Billymthetic preparation); SPOD
      Buoligical study); PREP (Preparation); UNES (Uses)
         apreprior from limbleid anid of; minichal and plant genes for
         .DELTA. 6-desuturases and their to in undreading traste levels of
         .domma.-line(Penir arid)
     +0- \pm \frac{1}{2}- \pm \frac{1}{2}, \pm \frac{1}{2}-Outladecadiencic (cid (C,Z -, relactions
ΙT
     BL: BOT (Reartant)
         a. dammaa. - Linolenic acid prepo. from; recrepiel and plant denes
         for .DEDTA.6-desaturases and their use in in reasing tissue
         levels of .camma.-linelenic acids
L24 ANGWER 5 OF 19 HOAFINS COPYRIGHT 1:37 ACS
1997: LS. 81 | Sociament No. 128: 39444 | Temperature-regulated mRNA
     accumulation and stabilization for fatty acid
     desaturase genes in the syanchasterium Nymechococces sp.
     strain FOC TIVE. Sakamote, Tecnio; Fryant, Dinald A. (Department of
     Blochemistry and Molecular Bic. Egy, The Fennsylvania State
     University, Thispersity Bard, PA, 168-8, UVA). Not. M. Eribiol.,
     . 5(+), 12-11-12-20 (English) 1994. COMEN: MOMIEE. ISSN: 1950-9-22.
     inddiaher: Blazawell.
AB
     Cyanobacteria applimate to low-temp. Conductions by desaturating
     thour membrano lipida. The de.B. .coega.: desaturase, and desC
      1.DELTA.9 desaturase) games of Symbolic objects sp. strain ECC 7002
     werk cloned and characterized, and the empression of the desA (.
     DELTA.12 desaturase), desB and desC denér was
     intudied as a function of temp. The steady-state mEMA abundance for
     the desA gene was threefold nigher in colls group at M2.degree.C
     than in calls grown at 38. decree.C. Desk transcripts were not detected at 85. degree.T, but were abundant in calls grown at
     .2.degree.3. Devels of dead madA were similar at both growth temps. The madA levels of each desaturase gase increased within 15 min of a
     temp. snift-gown to 22.degree. 1, and reMA level, recovered within 15
     min after a shift-up to 38.degree.C. The sold-induced accumulation
     of transcripts from the derA and desh pends was suppressed by the
     addr. of chloramphenical, but the transport elecation of the desC
     transcript levels at 22.degree.C was not affected by
     chloramphenical. The half-lives of the desA and desB mENAs were significantly longer in cells grown at 2. degree. I than in cells grown at 38.degree. I, but the desC mENA had a similar half-life at
     both temps. These studies reveal three patterns of temp. regulation
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for the desaturase genes, whose expression is tightly controlled by
     a combination of mRMA synthesis and stabilization. These studies
     demonstrate that elevation of desaturase mRNA levels is not the
     nate-limiting event during the low-temp, addlimation of
     cyanobasteria.
     16-1 (Microbial, Algal, and Fungal Biochemistry)
     Section or ss-reference(s): s
     Stme madebata fatty acid desaturase
     gene se pance
     Gemes (miprobial)
     RI: PEP - Properties'
         desA; temp.-regulated mEMA accumulation and stabilization for
      fatty acid desaturase genes in
        yan drasterium Synechococcus sp. strain POC 7002)
     Genes (migrobial,
     Fil: FRP 'Properties'
         wash; temp.-regulated mEMA abdumulation and stabilization for
      fatty acid desaturase genes in
        manulaiterium Synechodoccus sp. strain PCC 7000:
     Genes (mibrobial)
     FD: ERF /Properties
         desC; 'emp.-regulated mEMA accumulation and stabilization for
      fatty acid desaturase denes in
        syanold sterium Synechoologus sp. strain PCC 7002)
     SIA segiten es
     Erotein despendes
     Byrandha wanda
     Temperature effects (beological)
         temp.-regulated mELVA argumulation and stabilization for
      fatty acid desaturase genes in
       oryanchasterium Syneshopsopus sp. strain PCC 7001.
    mE.NA
     Fig. IPP (Properties)
        themp.-regulated mANA accumulation and stabilization for
      fatty acid desaturase denes in
        cyanchacterium Symeonopolocus sp. strain PCC 7301,
     156532-36-4
     ED: PFF (Properties)
        faming acid sequence; temp.-regulated mENA accumulation and
        stabilination for fatty acid
      desaturase genes in cyanolacterium Synechoococus op.
        ntrain FCC 7002)
     153463-19-1, GenBank D15773 183176-13-2, GenBank U36389
     109176-00- , GenBank Us689
     FI: FF + Properties.
         nucles ide sequence; temp.-regulated mENA accumulation and
        stabilization for fatty acid
      desaturase genes in cyanomacterium Symethocologus .p.
       mrain 100 7002)
     30 14-34-0, Fatty acid desaturase
     El: IFP (Properties,
        -temp.-regulated mENA argumulation and stabilization for
      fatty acid desaturase denes in
        cyanobisterium Synechschoodys sp. strain FOC 710.
L24 ANDERF 6 OF 19 HOAPLUN COPYRIGHT 1997 ACS
1996:7 Deciment No. 126:115911. The F-OLE1 gene of Pichia angusta
     endomes a .DELTA.9-fatty acid desaturase
     and complements the old mutation of Sappharemyces
     corvisia. Anamnart, Sarintip; Tomita, Tetsishi; Fukui, Fumio;
     Pujumori, Mo; Harashima, Satoshi; Yamada, Yasuniro; Oshima, Yasuji
     (Department of Biotechnology, Faculty of Engineering, Osaka
     University, 2-1 Yamadaoka, Suita-shi, Osaka, 965, Japan). Gene,
     104(2), 290-306 (Engli h) 1997. CODEN: GENED6. ISSN: 0578-1119.
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Publisher: Elsevier.
AB
     Three PCR-amplified DNA fragments appridizing with the OLE1 gene
     encoding .DELTA.9-fatty acid desaturase
     of Saccharomyces cerevisiae were obtained using, resp., genomic DNAs
     of one strain each of Kluyveromyces thermotolerans, Pichia angusta
     and Yurrowia lipolytica as templates. A gene designated P-OLE1 was
     cline! from the above fragment of P. angusta and sequenced. An open
     teading frame of P-DLB1 encodes a 44.6-kDa protein consisting of 451
     amino abid residues, which shows high identity (62) and similarity
     (19) to that deduced from the OLEI hadleotide sequence. Expression
     of P-ODE1 driven by the Q. derevisiae GAP promoter or its own
     primiter complemented the olel mutation of S. derevisiae.
     Transpription of 9-0LE1 in the native host was suggested to be
     partially repressed by cleic acid in the medium, as was that of OLE1
     in S. derevisiae and a similar year in Y. lipolytica, but that of a
     similar gene in W. thermatolerans was not.
CC
     3-3 (Bibmhemidal Genetics)
     Section pross-reference(s): 7, 10
ST
     POLE1 gene fatty acid desaturase
     sequence; Fichia fatty acid desaturase
     gene sequence
ΙΤ
     Genes (midrebial)
     EL: ANT (Analyte): BPR (Biological process): BPP (Properties): ANST
     (Analytical study); BIOL (Biological study); PROC (Process)
        (E-DLE1; the P-OLE1 gene of Pichia angusta encodes a .DELTA.9-
      fatty acid desaturase and complements
        the oled mutation of Saccharemydes cerevisiae.
TT
     Erotein sequences
        (ci Pichia angusta .DEDTA.9-fatty acid
      desaturase 7)
TT
     DMA sequences
        (of the F-OLE1 gene of Pichia angusta encoding a .DELTA.9-
      fatty acid desaturase and
        complementing the blel mutation of Sadbhardmydes
        cerevisiae)
IT
     Bichia angusta
     Saccharomyces cerevisiae
        (the P-CLE1 gene of Pichia angusta encodes a .DEDTA.9-
      fatty acid desaturase and complements
        the olel mutation of Saddhardmydes derevisiae)
     112-36-1, Cleic acid, biological studies
     FL: BAT (Biological activity or effector, except adverse); BIOL
     (Fiological study)
        (E-OLE) gene of Fighia angusta encoding a .DEDTA.9-fatty
      acid desaturase and complementing the olel
     mutation of Sadoharomydes derevisiae repressed by oleic
        acidi
IT.
     186208-06-0:
     FI: EAC +Biclogical activity or effector, except adverse); PRP
     (Froperties); BIOL (Biological study)
        (arino acid sequence; the P-OLE1 gene of Picnia angusta encodes a
        .16 NPA. 3-fatty acid desaturase and
        complements the ilel mutation of Saccharomydes
        perevisiae)
ΙΤ
     186209-56-3
     EL: FEE (Properties)
        (nublectide sequence; the P-OLEI gene of Pichia angusta encodes a
        .OFLTA. 3-fatty acid desaturase and
        complements the olel mutation of Saccharomyces
        cerevisiae)
ΙT
     9(14-14-0), .DELTA.9-Fatty acid
     desaturase
     RL: BAC (Biological activity or effector, except adverse); PRP
     (Properties); BIOL (Biological study)
                           RATHLEEN FULLER BT/LIBRARY 305-4290
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(the P-OLE1 gene of Pichia angusta encodes a .DELTA.9fatty acid desaturase and complements the olel mutation of Saccharchydes deravisiae) L24 ANGWER 7 OF 19 HOAPLUS COPYRIGHT 1997 AGS Document No. 124:319.95 Isolation and characterization of an Arabidopsis thaliana dDNA encoding a .DEUTA.7-sterol-0-5-departurase by functional complementation of a defective yeast mutant. Gasnotte, Daniel; Husselstein, Pania; Bard, Martin; Lasroute, Francois; Benveniste, Puerre (Department de Biologie Cellulaire et Moleculaire, Institut de Botanique, Strasbourg, 67033, Fr.). Plant 7., 9(3), 391-9 (English: 1996. CODEN: PLIVED. ISSN: 09-10-7412. A yeast hull mutant (erg 3) defective in BBO 3, the gene AB emboding the C-5 sterol desaturase required for ergosterol synthesis was transformed with an Arabidopsis thaliana cDNA library inserted in a yeast vector. Transformants (4. ines.10); were screened for cycloheximide (CE) resistance and 400 possible clones were analyzed to det. their sterol profile. Now levels of ergosterol in addn. to .DEDTA.7- and .DEDTA.8-stercls normally present in erg3 were is dated in three yeast transformants. Characterization of one transformant indicated a cONA of 1141 bp. Transformation of an erg fixtrain with this plasmid led to CH resistance, hystatin sensitivity and an ergosterol profile. After sub-cloning in a pBluescript vector and subsequent segmenting, an CBF of 643 bp en moding a possible 291 Amino acid polypoptide was deduced. Three histodine-rich motifs (HXEH, HXEHH and HXEHH) were found in the A. thaliana CRF which are also present in the yeast ESG 3 gene. These histidine-rich motifs are also characteristic of many membrane-bound fatty acid desaturases from nigher plants. These data strongly suggest that the A. thallana cONA endodes a .DELFA.7-steroi-C-3-desaturase. 3-3 (Piochemical Genetics) Section ordes=reference(s): 7, 11 ST Arabidopsis sterbl desaturase bDMA sequence gene ΙT Gene, plant FL: PPF (Eroperties) (for C-f stere) desaturase; is lation and characterization of Arabidopsis thaliana GDNA +nocding .DELMA.7-sterol-C-f-desaturase by functional complementation of defective yeast mutant Anabidopsis thaliana ΙΤ Protein sequences disclation and characterization of Arabidopsis thaliana cDNA encoding .SELTA.7-sterol-C-5-quasturase by functional complementation of defective yeast mutant. Deckyribonucleic acid sequences ΙT occumplementary, isolation and maracterization of Arabidopsis thaliana cDNA encoding .DEDMA. -store.-C-i-desaturase by functional complementation of defective yeast mutant) 175960-67-5 IT FL: PFF (Eropenties) amino acid sequence contq. conee hisridide-rich motifs; isclation and characterization of Arabicopsis thaliana cONA encoming .DBLTA.?-stertl-C-S-mesaturase by functional complementation of defective yeast mutant 372 5-37-1 EL: BUU (Biological use, unclassified); 5101 (Biological study); USES (Uses) isplation and characterization of Arabic psis thalians SDNA encoding .DELFA.7-sterol-C-f-desaturase by functional complementation of defective yeast mutant) ΙT 170611-11-7, Genbank X90454

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RL: PRP (Properties)

(nucleotide sequence; isolation and characterization of

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Arabidopsis thaliana cENA encodin: .DELTA.7-sterol-C-6-desaturase
        by functional complementation of defective yeast mutant
L24 ANSWER 3 OF 1+ HCAPLUS COPYRIGHT 1+47 ACS
1995:235599 Decument No. 137:750997 Molecular cloning of cDNA for
     fatty acid desaturase of Anacystis
     midulans and its use in areating transgenic plant resistant to cold
     temperature. Nish:zawa, Osamu; Togu::, Toshihiro (Hirin Beer K. K.,
     Tapan). PCT Int. Appl. WG B518202 A1 950706, 41 pp. DESIGNATED
     STATES: W: AM, AU, BB, BC, BF, BY, CA, CU, CZ, FI, GE, HU, JE, KG, KE, KZ, LK, LT, LV, MD, MG, MH, MO, UL, PL, RO, RU, SI, SK, TI, TT, UA, US, UN, VH; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DE, ES,
     FE, GA, SB, GR, IE, IT, LU, NO, ML, NE, NE, NE, ET, SE, SN, TO, TG.
     (Japanese). ODDEM: PINKDE. APPLICATION: WO 54-JP2258 941228.
     PRIORITY: UP +3-353656 931233.
AB
     Gene des 9 var fragment of Anabacha variabilis IAM N-3 is isolated
     upstream in m gene desA that encodes .DELTA.-12
     -unsiturage and used as a probe for the isolation of open reading
     frame (ORF) des à nid if Anadystis nivulans. ORF des à nid bodes
     for a desaturase desaturating the .DFLTA. -position of a fatty acid
     Ecuna to a lipid and exhibits 50 and 30% similarity to gene des 9
     var of Anabaena variabilis and steam yl-C-A unsaturase of mouse,
     resp. In- OEF introduced int: transcenic tobacco plants increased
     the content of unsate, fatty acids and the resistance to cold temp.
     ICM CLIN I - A
IC
     103 | 012N00: -00; A01H00:-00; A01H00:-00
ICA CLEMOS9-0
CC
     Tell (Enlaymen)
     Section chows-reference(s): 1w
ST
     Anacystis fatty acid desaturase SDNA
     sequence; o la resistance des 3 mid Adacyutus; transgenic plant
     unsate fatty Adie
ΙT
     Gene, plant
     FL: AGE (Agricultural use); FRE Properties; BIOL Biological
     study); TDEN (Uses)
         uses 3 mid; obsming of oBMA for .IFLTA.9-fatty
      acid desaturase of Anacystis nigulans and its
        use in creating transferio plant is sistant to cold temp.)
     Erotein sequences
IΤ
         > f .DELTA. Hefatty acid desaturase
        or Amany-tis niquians
     Elarr. reli
IT
     Flant
     Tcbsabble
         transpenie; empression of cDNA for .DFLTA.9-fatty
      acid desaturase of Anacystis nichulant inc
IΤ
     Temperature effects, biological

    sold, empression of sollA for .DELTA.9-fatty

      acid desaturase of Anacysti, nidulancin
        transgenic plants to increase restrain ento)
ΙT
     Deoxyribonalleid atid sequences
         cromplementary, for .DELTW.9-fatty acid
      desaturase of Analystis miduland)
ΙΤ
     Pattly adids, misdellaneous
     RL: MSC (Miscellarwaus)
        Consat t., expression of cDNA for .DELTA. 3-fatty
      acid desaturase of Anacystic nitulans in
        transgemic plants to increase content of:
     168613-13-6
     FL: AGE (Agricultural use); PEP (Properties); BIOL (Biological
     study); UNES (Uses)
        (amino acid sequence; cloning of DNA for .DELTA.9-fatty
                            MATHLEEN FULLER BT/LIBRARY 308-4290
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acid desaturase of Anacystis nidulans and its
        use in creating transdenic plant resistant to cold temp.)
     166372-04-3
TT
     Ph: AGE (Agricultural use); PRF (Properties); PIOL (Biological
     study); USES (Uses)
        (nucleatide sequence; claning of cDNA for .DELTA.3-fatty
      acid desaturase of Anacystis midulans and its
        use in preating transmenic plant resistant to cold temp.)
L24 ANSWER + OF 19 HOAPLUS COPYFIGHT 1997 ACS
1995:27:449 Document No. 127:29803 Identification of a gene that
     complements an Arabidopsis mutant deficient in chloroplast
     .cmedi.desaturase activity. Falloome, Deane L.; Gibson, Susan;
     Demieux, Bertrand; Somerville, Chris (Dep. Plant Biol., Carnegie
     Inst., Stanford, CA, 94816, USA). <u>Plant Physic1., 108(4), 1453-9</u> (<u>English: 1344.</u> COOEN: PLAHAY. ISSN: 0682-0889.
    Meriprane lipteds of the fade (formerly fade) mutant of
AΒ
    Arabado, sis, which is deficient in chloroplast .cmega.6 desaturase
     activity, have increased levels of montunsated. fatty
     acids and are deficient in trienoid fatty
     acids. A gitative face cDNA clone was isolated by probing a
     COMA library with a degenerate oligonuclectide based on a conserved
     region within known .cmega.3 desaturase genes. Expression of the
     cENA in transgeried plants of a fad6 mutant restored normal
     levels of all fatty acids. When used as a
     hybridication prope, the cSMA identified a restriction
     fragment-length polymorphism that po-sagregated with the fade
    mutation. Thus, on the basis of a genetic complementation
     text and genetic map position, the fad6 dene is encoded by the cDNA.
     The GIMA encoded a 415-amin: soid polymeratide of 47,7.7 D that
     displayed a high degree of segmente similarity to a .DELTA
     .12 desaturase from the Tyanobacterium Synechocystis. The
     facé mene exhibited less sequence nomo), to any known higher plant
     desir druse, including an endoplasmic retibulum-locatioed .omega.6
     desaturase corresponding to the Arabidopsis fad2 gene.
     7-5 :Encymes.
CC
     Septian pross-reference(b): 3, 11
ST
     fatty acid Diegal desaturase sequence
     Arabidopwis; cDNA omegaé desaturase sequence Arabidopwis
     chibroplast; genw fadd swquence omaga6 desaturase Arabidopsis
ΙT
     Gene, plant
     E.L.: PEP (Properties)
        (tage; identification of gene that complements Arabidopsis
      mutant definient in onloreplast .omega. o desaturase
        setimaty)
TΤ
     Arab. dopsis inaliana
     Chi moplast
     I.e. f
     Protein sequences
        (.gentification of gene that complements Arabidopsus
      mutant deficient in emboroplast .bmega.n desaturase
        antivity)
     Fatty acids, biological studies
TT
     RA: BOC (Biological omnumence); MFM Metapolic formation); BIOL
     -Booled sal study); FDFM (Formation, nonpreparative); OCCO
      Odd.rr-ndet
        understiffication of gene that complements Arabidopsis
      mutant deficient in emberoplast .omega.6 desaturase
        a:timity)
ΙT
     Deoxyriponurleic acid sequences
        complementary, identification of gene that complements
        Arabidopsis mutant deficient in chloroplast .omega.6
        desaturase activity)
     163961-98-6
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PL: BAC (Piological activity or effector, except adverse); PRP
      Properties); BIGL (Fislogical study)
         didentification of gene that complements Arabidopsis
      mutant deficient in chloroplast .emega.6 desaturase
         activity)
     (6819-61-4, Fatty acid .cmera.6+
ΙT
     Desaturase
     FL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL
     -Biological study); FOEM (Formation, nonpreparative); OCCU
      (economic femera)

    identification of gene that complements Arabidopsis

      mutant deficient in the riplast lomedalo desaturase
      108670-84-6, GenBank VD9 08
ΙT
     Fil: PF.P (Froperties)
          nurlection sequence of; identification of seme that complements
        Arabidopsis mutant deficient in chloroplast .omega.6
        Hesaturase activity)
L24 MISWER 10 OF 19 HOAFLUS COPYRIGHT 1997 ACS
1995:1 1174
              Lucument No. 127:174542 Oloning of .meda.F desaturase
     from dyampharteria and its use in altering the degree of
     rambrane-lipid insaturation. Sakanoto, Toshio; Los, Dmitry A.;
     H.qashi, Choichi; Wada, Hattme; Nishida, Ikuo; Ommori, Masayuki;
     Murate, Mirio (Department Mulecular Biome manits, Graduate
     Thirefairy Advanced Studies, Okazaki, 444, Japani. Elant Mol.
     B.:1., 26<sup>2</sup>1), 249-x3 (English) 1934. CODEN: PMB10B. ISSN:
     (16.4-441.
    Cyanobacteria respond to a decrease in temp. by desaturating
AB
     fatty acids of membrane lipids to compensate for
     the door ase in membrane fluidity. Among various desath, reactions
     in Hyanobarteria, the decath. of the Lomega.3 position of
     fatty acids is the most censitive to the change in
     temp. In the present study, the authors isolated a gene, designated design, for the immegal: desturase from the symmetry,
     Symmetric sp. FCC 6808. The desB gene encodes a protein a 359 and no-actual residues with mil. mass of 41. kDa. The desB gene is transcribed as a menodistronic operen that produced a single
     transcript of 1.4 dr. The level of the dosh transcript in cells grown at .7.degree, was 10 times higher than that in cells grown at
     14.degre-.. To manipulate the fatty-acid
     unsath. It membrane lipids, the desB gene in Symeonogyatis sp. PCC
     fifth was mutated by insertion of a kanamydin-resistance
     gene cartings. The resultant mutant was unable to
     desaturate fatty acids at the .omega. ?
     pasition. The desA gene, which encodes the .DELTA.

12 deaturase of Syndonicystis sp. PCC 6810, and the desB gene were introduced into Syndonococcus sp. PCC 7842. While the
     parent by modasterion can only desaturate membrane lipids at the
     .DELTA. 9 pesition of fatty acids, the resultant
     transformant was able to desaturate fatty
     acids of nomerane lipids at the .DELTA. 3, .DELTA.
     12 and . sega. Postions. These results confirm the
     thin time, it the deals generally demonstrate that it is possible to
     opinetically manipulate the fatty-acid unsath. of
     fembrane lipids in cyanoba teria.
CC
     5-3 (Biodhemigal Genetids)
     Section mass-reference .): 7, 10
ST
     cloming a quence omegas desaturase gene Synech dystis; Synechocystis
     d-saturable alteration membrane lipid unsain; done desB sequence
     ome (a) delaturase Synephopystis; transcription omegab desaturase
     gene Synephocystis temp; desaturase delta: 2 omegas Synephocystis
     transformation Symechococcus
ΙT
     Symechicoccus
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```
Transformation, genetic
         alteration of membrane lipid unsath, in Symethococcus sp. FCC
        T941 by transformation with .omega.3- and .DELTA.
      12 desaturase genes from Synechopystis sp. F00 6803
ΙT
     Lipids, biological studies
     RL: MFM (Metab dis formation); BIOL (Biblidical study); FORM
     (Formation, nonpreparative)
        (alteration of membrane Lipid unsath, in Synechopsocous sp. FCC
        7 M. by transformation with .omega.3- and .DELTA.
      12 desaturase genes from Synechopystis sp. FGC 6813:
ΙT
     Fatty acids, brological studies
     RL: MFM (Metabolic formation); BIOD (Biblogical study); FORM
     ·Formation, numpreparative:
        (changes in fatty acid compn. of total ligids
        uppn transformation of Symechoporous sp. E73 7942 with .omeda.3-
        and .DELTA.12 desaturase genes from
        Symmonicystis sp. ECO 6303)
IΤ
     Syne thooystis
        (nlining and sequence of .omega.) desaturage from Syneithococous
        and its use in altering the degree of membrane-lipid unsath.)
ΙT
     Cell mambrane
     Decayribonicleso acid sequences
     Emotoin sequences
        (a) which and sequence of comegati desaturase from Symeohodystis
        and its use in altering the degree of membrane-lipid unsath.)
IT
     Cyanobacteria
        (oloning and sequence of .omega.) desaturase from cyanobacteria
        and its use in altering the degree of membrane-lipid unsath.)
     Gene, miarabia.
ΙT
     FL: BPR (Biological priness ; PRR (Properties ; BIOL (Biological
     study); PROC (Process)
        class; claning and sequence of .imega.f desaturase wene desb from
        Symechococcus and its use in altering the degree of
        menurane-lipid unsath.)
     Temperature effects, biological
TT
        (temp. regulation of limegal) desaturase gene desb transcript
        I vels in Symechologistus:
ΙT
     Ribonicheid adias, messender
     FL: MPM (Metabolic formation); BIOL (Biological study ; FORM
     (Formation, nonpreparative)
        ctomp. regulation of .omega.2 desatirase gene desatiransdript
        l vels in Synechocystis)
IT
     Cene, microbial
     FL: PPF (Miological process); BICL (Biological study); PROC
     (P20 %.33)
        rosesA, .DELTA.12 desaturase; alteration of
        moderane lipid unsath. in Synephologopus sp. ECC 1949 by
        transformation with .omega.3- and .DELTA.12 \,
        a saturase genes from Symethopystis sp. PCC 6808)
     7253 - 15-1, .DELTA.12 Dematurase
ΙT
     FL: RAC (Piological activity or effector, except adverse); BIOL
     (Bible sical study)
        calteration of membrane dipid ensata, in Symethologous sp. PCC
        14. by transformation with imaga. i- and .DELTA.
      12 Webaturase genes from Synechopystis sp. E20 6303
IT
     7-1 -3, Hexadedanbid agud, biològical studies
                                                       57-11-4, € 18:0,
     tiological studies (3-53-4, \theta,1\chi-Optadepadienord adid (2,3)-,
     tiological studies 112-50-1, 3-Octadecenoic acid 20-, studies 373-49-3, 9-Hexadecenoic acid, (Z)=-463-40-1
                          113-50-1, 9-Octadesenoic acid Ju-, biological
     11-0 made sension and (2)- = 5070-(3-1, 9,12-H wadecadiencie acid,
     Z_1Z_2 + Z_3 + 34 - 77 - 2, Obtade sadienvid abid (Z_1Z_2) - 328 + 9 - 24 - 0
     EL: BOC Biological occurrence); MFM (Metabolic format.on); BIOL
     Biological study); FORM (Formation, nonpreparative); OCCU
     (Occurrence)
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KATHLEEN FULLER BT/LIBEARY 308-4290

```
(changes in fatty acid compn. of total lipids
        upon transformation of Dynechoppopus sp. 200 7942 with .omega.3-
        ah:: .DELTA.12 desaturase genes from:
        Symechocystis sp. PCU 6803)
     7142^{6}-14-4, .DELTA.15 Desaturase
ΙΤ
     161027-24-3
     PL: BAC (Biological activity in effector, except adverse); PRP
      Properties); BIOL (Bislemeal study)
        coloning and sequence of .omega.b desaturase from byanobacteria
        and its use in altering the degree of membdane-lipid unsath.
     1.002.14-15-7
ΙT
     FL: BPS (Piplogical process); PRP (Properties); BICL (Biplogical
     roudy : PRAG (Erodess)
        ordening and sequence of .emega.b desaturase from cyanobacteria
        and its use in altering the degree of membrane-lipid unsath.
L24 ANSWER 11 OF 19 HCAPLUS COPYRIGHT 1997 ACS
1994:057337 | Isrument No. 121:097399 | Altering the linclenic and
     limpleid adia content of plant pils by altering the levels of
     Innoleic word desaturase. Gibson, Susan Irma; Kishore, Banesh
Burthy; Euff, Thomas Gene; Somerville, Christopher Roland; Arondel,
     Monocht (Wan-Marie Armel Monsanto Co., USA; Michigan State
     University). FOT Int. Appli WO 9418337 Al 940818, 143 pp.
1083(CHATE) STATES: W: CA, TE, TS, US, EW: AT, BE, CH, DE, DK, ES,
FR, CB, GR, IE, IT, DU, HH, NS, PT, SE. (English). CODEN: PIXXD2.
     APPLICATION: WO 94-US1321 040204. PRIORITY: US 93-14431 930205; US
     ···-1:..:51 9:31122.
     The linchenic sold content of vegetable oils is altered by changing
AВ
     the levels of expression of linoleic acid desaturase, e.g. by
     expression of a heterologius gene or antisense gene for the enzyme.
     A cDMA for the enzyme derived from the fad3 game of Brassica napus
     was introduced into wild-type and fadl mutants of
     Agabodingsis thalians by Appelbacterium-mediated transformation and
     transferit plants prepd. Transformation of the wild type increased
     the linclemate content from 31.9.4-.4.5 to 51.5.4-.10.9 moly of
     fatty acids and in the fall mutants the
     undrease was from 6.7.+-...? to 48.1.+-.15.5 molt of fatty
     acids.
     TOM 013NT15-34
IC.
     ICS ("12N 15-53; 012N315-11; 012N135-11; A01H365-83; 051B361-00
     11-1 Blant Birchemistry
CC
     Shatika diaserteferendeka : 3
ST
     linoleate desaturase plant linoleic acid level
ΙT
     Adabidiyasa thaliana
        (fig) were of; alteriar the limplenic and limbleic acid content
        or plant cils by altering the levels of linoleic acid desaturase)
ΙT
     Gene, plant
     HD: Bloth (Birliginal study)
        (tadi, for limbleate downturase of Brassica mapus; altering the
        limitenic and limblete abid bontent of plant bils by altering the
        levels of limbleic and desaturase)
     (ene, flant
T. T.
     PL: BELL Fielggigal et alg
        (1955, of Arabidopsis thalsans; altering the liroienic and
        linities, additiontent of plant bils by altering the levels of
        linglace acid desaturace)
TT
     Gene, plant
     EL: BIBL Bibliogical study
         (tadD, for lincleate desaturase of Arabidopsis thaliana; altering
        the linclenic and lincleic acid content of plant oils by altering
        the levels of linoleic acid desaturase)
ΙТ
     Gene, plant
     EL: BILL (Biblogical study)
        tfadE, for lincleate desaturase of Arabidopsis thallana; altering
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the linolenic and lincleic acid content of plant oils by altering
        the levels of linoleic acid desaturase
     Protein sequences
ΙT
        (of lineleic acid desaturases of Arabidopsis and Brassica)
ΙT
     Plasmid and Episome
        (pMON1:301, pMON1:300), expression vectors for plants; altering
        the linclenia and limbleid acid content of plant bils by altering
        the levels of linclers acid desaturase:
     Plasmid and Episone
ΙT
        (pMON1:804, pMON18800, Brassida napus lincleate desaturase
        antisense gene on; altering the limplemic and limpleic acid
        content of plant cits by altering the levels of linoless acid
        desaturase)
ΙT
     Plasmid and Episome
        q-TiDEC3, Brassida napus linoleate desaturase gene on; altering
        the limelenie and lumbledo abid bontent of plant oils by altering
        the levels of lincheld acid desaturase
ΙT
     Plasmid and Episome
        griffeth, limpleate desaturase wene of Arabidopsis thaliana on;
        altering the lindlenge and lindleid add content of plant oils by
        altering the levels of lincleic acid desaturase)
    Fape | plant)
     Seed
     Soykman
        of ranscanic; altering the limblenic and limbleic acid content of
        plant oils by altering the levels of limpleic acid desaturase)
     Flamt stress
ΙT
        coold, improved resustance to; altering the limblenic and
        luncheid adia content of plant oils by aftering the levels of
        lincleic acid desaturase)
     Leomyribonualeir said sequences
ΙT
        (complementary, for limited acid desaturases of Arabidopsis and
        Boassidar
     Leamuribinudleic soids
IΤ
     FL: PUT (Riplemental ise, unclassified); 5:01 (Fiological Study);
     USES TRAFFI
        (complementary, antisense, to fad3 gene for limbleate desaturase
        :: Arabidopsis thaldana; altering the dinclenic and lindleic acid
        content of plant rils by altering the levels of linolete acid
        desaturase)
ΙT
    Mibroorganism
        qhytopathogenic, improved resistance to; altering the Linolenic
        and lincleic acid content of plant bill by altering the levels of
    lineleic adid deseturase)
Fats and Clyperidic file
     FL: PMF (Bidingustrial manufacture); PRP Properties); BICG
     (Biological study); EEEE (Preparation)
        cregetable, altering the linelenic and lineleic acid content of
        plant oils by altering the levels of linoleic acid desaturase)
     112-x1-1, 9-Octa-becenoid adid (2)-, biological studies
     Pinolenio acid 3062-16-0, Linoleio acid desaturase
     FL: AGR (Agricultural ase); MEM (Metaboli: (crmation); BIOL
     (Biological study): FORM (Formation, compreparative): USES (Uses)
         Saltering the limblemic and limbleic adia content of plant oils
        by altering the levels of limbleid adid desaturase)
ΙΤ
     148814-49-7 149955-97-5 158651-91-3
     EL: AGE (Agricultural use); PEP (Properties); BIOL (Biological
     study); USES (Tses)
        mino acid sequence; altering the limblenic and limbleic acid
        menters of plant oils by altering the levels of linoleic acid
        desaturase)
17
     7142'-(4-8, .DELTA.15 Desaturase
     EL: AGE (Agricultural ase); BOC (Biological occurrence); PRP
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(Properties); BIOL (Biological study); OCCU (Occurrence); USES
        cloning of Arabidopsis thalians gene for; altering the linolenic
       an: limiteid adid content of plant oils by altering the levels of
        finel-ic acid desaturașe)
     IT
     EL: AGF (Adricultural use); PEP (Properties); BIOL (Biological
     study,; TSES (Uses,
        'hurl-otide sequence; alt- mind the dinolenic and linoleic acid
       content of plant oils by altering the levels of linoleic acid
       desaturase)
L24 ANOMER 10 OF 19 HOREING COPYRIGHT 1997 ACS
1994: 620640 Discument No. 121: 226640 Molecular cloning of dDNA for
    mi mesernal delta-12 fatty acid
     desaturases and their use for molepular breeding of plants.
     Lightner, Jonathan Edward; )Oculey, John Joseph (du Pont de Nemours,
     E. I., and Ci., USAO: FOT Int. App). WO 411518 A1 340526, 147 pp.
     DELIGNATED STATES: W: AU, BE, CA, CA, DS, EW: AT, BE, CH, DE, DK,
     ES, SH, GB, GR, IE, IT, DU, DY, ND, ST, SE. (English). CODEN:
     EDUNCAL. APPLICATION: WO 9:-1399:7 9:1013. PRIORITY: US 92-977339
     921117.
    The prepr. and use of nucleic axid fragments encoding fatty
ΑВ
    acid desaturases and related ensymes are
    described. The invention permits alteration of plant lipid compo.
    Chineric genes incorporating such nucleic acid fragments with
     surtable regulatory sequences may be used to preste transgenic
     plants with altered levels of unsato, fatty acids. The ploning of
     cDNA for fatty acid .DELTA.12
     -desaturases (identil-Ocal desaturases) from Arabidopsis
     theliana, Brassida napūs, Glytine mak, Zea mays, and Ricinus
     communi: was demonstrated. The expression/of antisense G. pax
     fatty acid .DELTA.12-
     desaturase cDNA in scybeans to reduce the expression of the
     ensyme in developing scybean seeds and use of the oDNA sequences for
     restriction fragment length polymorphism. RFLP) mapping was also
    demonstrated.
IC
   104 0121013-53
    TO: 012:015-82; 0118001-0 ; 0120001-68; A018005-00
    11-1 (Elant Biochemistry)
CC
     Section pross-reference(s): z_{i} 17
    plant fatty acid desaturase -2NA
     oloning; breëding lipid domph transgenic plant
ΙT
     Plant breeding and selection
        Friening of fatty acid desaturase
       willA in relation to)
IΤ
    Candla
     Soldie an
        -fatty acid desaturase empression
        in, antigense diMA for redn. of (
ΙT
     Profein sequences
        "of plant midrosomal fatty acid
     desaturases)
ΙT
     Planmid and Episone
        piPh tea2a, p2000a2a, p2K ted2k, fatty acid
      desaturase antisette cONA of Brassica napus on, for
       expression redn.)
ΙT
     Fatz and Olyceridic bils
     RL: FEP 'Properties)
        itran menic plant cells having altered level of, cloning of
     fatty acid desaturase in relation to)
IΤ
    Pla:it
        stranggenic, unsatd. fatty acid level regulation in, cloning of
       cDNA for fatty acid desaturase in
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relation to)
     Deoxyribonuble id adid sequences
        (samplementary, for plant microsomal fatty acid
      desaturases)
ΙT
     Deckyriborusleis asids
     FL: BIOL (Biological study)
        * samplementary, antisense, for fatty acid
      desaturase, for reducing desaturase gene
        empression in transgense plants)
ΙΤ
     Flasmid and Episome
         p3711, fatty acid desaturase
        antisense oDMA of Glycine max on, for expression redn.)
ΙΤ
     Genetic bolymorphism
        restriction fragment length, Genetic mapping, of gene for
      fatty acid desaturase of plants,
        sleding of fatty acid desaturase
        SOMA in relation to)
ΙT
     Farty abids, blological studies
     PL: PRE (Properties)
        funsatd., transgenic plant cells having altered level of, cloning
        of fatty acid desaturase in
        relation to:
     158283-24-0, .delta.-12 Fatty
ΙT
     acid desaturase (Arabidopais thaliana clone
     #9.1131 158283-26-2, .delta.-12
     Fatty acid desaturase (Prassica napus
     clone pCF2-1650) 158283-28-4, .delta.-12
     Fatty acid desaturase (Glycine max clone
     pSFM-16HM 158283-30-8, .delta.-12
     Fatty acid desaturase (Zea mays clone
     pFadl#1) 158283-32-0, .delta.-12
     Fatty acid desaturase (Ricinus communis
     clone pEF2-10) 158283-34-2, .delta.-12
     Fatty acid desaturase (Riginus communis
     close pEF1970-42)
     FL: BIOL (Biological study)
        tamino acid sequence of and cloning of cDNA for, mol. breeding in
        relation to:
     77~{\rm fb}^{\prime} - 95 - 9. Batty acid .DELTA.12-hydroxylase
ΙT
     FL: BICL (Bithodical study)
         Gene for, method for aloning of)
     84 (A) (1 - 91 - 3
ΙT
     BL: BIGE (Biological stody)
     (gene for, of plants, method for bioning of)
1543-33-33, RNA (Arabidopsis thatians dione pAGF2-6 .delta.
ΙΤ
     -12 fatty acid desaturase
     ger.e.,
     FL: BIGL (Biological study); PRP (Propert.es)
         nurlectide sequence and cloning of (
ΙT
     15. 110-16-7, 100A (Arabidopsis thaliana clone p92103 .delta.
     -12 fatty acid desaturase
     cDMA and flanks) 153283-25-1, DMA (Bras ica napus clone pCF2-165D
     fatty acid desaturase cDNA and flanks)
     1550-3-27-3, DWA (Glypine max plone p2F2-16TK .delta.-
     12 fatty acid desaturase GDNA
     and :lanks) 19:283-29-5, DNA (Zea mays -:lone pEad2#1
     .delta.-12 fatty acid
     desaturase cDNA and flanks) 158283-81-9, DNA (Ricinus
     communis clone pRF2-10 .delta.-12 fatty
     acid desaturase cDNA and flanks) 158283-55-1,
     DNA (Ricinus communis clone pRF1970-42 .delta.-12
     fatty acid desaturase sEWA and flanks)
     kL: BIBL Biological study); PRP (Properties)
        (nucleatide sequence and cloning of, mol. breeding in relation
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to) TT 141-12-7, Ricinoleic acid FL: PEP (Properties) (transgenic plant cells having altered level of, cloning of fatty acid desaturase in relation to) L24 ANSWER 13 OF 19 HOAPLUS COPYRIGHT 1997 ACS 1994:6349%L Disdument No. 121:324%ED Arabidopsis FAD2 gene encodes the ensyme that is essential for polyunsaturated lipid synthesis. & calley, John; Lighth r, Johathan; Feldmann, Henneth; Yadav, Marenira; Tark, Ellen; Browse, John (Inst. Bool. Chem., Washington State Univ., Pullman, WA, 491/4-6340, USA . Plant Cell, 6 1), 147-79 (Endlish) 1994. CODEM: PICEEW. 138N: 1940-4631. AΒ The polyunsata, fatty acids limoleate and salpha.-limolenate are innormant membrane components and are the essential fatty acids of human nurrition. The major ensyme responsible for the synthesis of these compiled is the plant pleate desaturase of the endoplusmic reticulum, and its activity us controlled in Arabidopsis by the fatty acid desath. . (fad. . brus. A fail all le was identifies in a population of Arabidopsis in which mutations had been created by T-DNA insertions. Genomic BNA fQ in constant the I-DNA was blocked by planmid resome and used to isolate CDNA was genomic closes of FADS. A CDNA contq. the entire FADS coding sequence was expressed in face mutant plants and shown to remplement the mutant factly acid phenotype. The on subeducting acid requency from the SDMA snywed homel, to other plant departurases, and this confirmed that PAD2 is the structural gene for the desaturase. GeT blot analyses of FAD2 mBNA bovels showed that the gene is expressed throughout the plant and suggest that transcript devels are in excess of the amt, needed to account for cleare desath. Jequence anal. Identified histidine-rich motifs that scula sentrabute to an area binding site in the cytoplasmic comain : the protein. Such a position would facilitate interaction between the desaturage and synthhromo bt, which is the direct source of electrins for the desard, reaction, but would limit interaction of the active site with the fatty adul substrate. CC 7=1. Encyones≀ Section gross-reference(s :) gene FALL pleate desuturase coquence Arabidopsis; cDNA FALL cleate ST desaturasé seguence Arabidopois ΙT Arabicopsis thalland Arabadopsis BADD gene for obeate desaturase that is essential for polymnsatd. Lipid synthesis) ΙT Ceno, plant FI: BIOL (Biological study 'FAD:; Arabidopsi: FAD: gene for eleate desaturase that is essential for polyunsatu. Lipid synthesis: ΙT To myrikomusleis acud sequences and Amaricopsus FAD2 game for oleate dosaturase) IΤ Endyna minotional sines Pritein seguences o: Adabidopals PND2 olgato desaturase ŢΤ 80 t. 2-3:-1, Oleate desaturise FL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological Study) (Arabidopsis FADU dene for oleate desaturase that is estential for polyunsatd. Lipid synthesis) ΙT 158283-24-0, Oleate Resaturano Arabidopsis thaliana clone pF.1 (en) (FAD2) EL: PEP Properties: (amin) arid sequence; Arabidopsis FAD2 gene for bleate desaturase that is assential for polymeath. lipid synthesis) ΙT 10241 - 10-7FL: PRP Properties)

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(nucleotide sequence; Arabidopsis FAD) gene for cleate desaturase that is essential for polyunsatd, lip.d synthesis) L24 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 1937 ACS 1994:474830 Dominant No. 121:74%30 Identification of conserved domains in the .DELTA.12 desaturases of dyanobacteria. Cakameto, Toshic; Wada, Hajime; Niskida, Ikuo; Ohmori, Masayuki; Murata, Morro (Dep. Mol. Bromechan., Univ. Advanced Studies, Okazaki, 444, Japan). Plant Mol. B.cl., .4(4), 643-50 (English) 1994 CODEN: PMBIDE. ISSN: 0107-441.. ΑВ Cyanobacterial genes for engages that desaturate fatty acids at the .DELTA.12 position, designated desA, were isolated from Symechocystis FCC6714, Cynephococcus POC7002 and Anabasma variabilis by cross-hybridization with a DMA probe derived from the desA dene of Symechodystis FCC6:03. The genes of Symuchomystis PCC6:14, Symechologopus PCC7002 and A. variabilis encode proteins of 349, 34% and 330 amino acid residues, rusp. The transformation of Symechadologs PCC7942 with the desA demes from Symetholystis FCCv714, Symethocopous FCC7002 and A. variabilis was assled, with the ability to introduce a second whole bond at the .DELTA.12 wesition of fatty acids. The amino acid sequence of the products of the desA denes revealed the presence of four conserved demains. Since one of the conserved domains was also found in the amine acid secrences of .imega.l desaturases if Brassina hapus and mung bean, this domain may play an essential role in the introduction of a double bond into tatty acids bound to membrane lipids. R-R (Fighterical Genetics) CC Jection pross-reference(s): 7, 11 dosaturase dene dewA sequendo cyancha teria; Amahaena Synechologocus ST Dyrochomystis desaturase gene sequence ΙΉ Amabaema variabilis (desaturase gene desA of, updated mislectide sequence of) ΙΤ Jyruscheeseaus Synarch boystis (dene desA of, ruplestide and encoded peptide sequences of) Decembracheir and sequences ΙT ouf desaturase dene desA, or Symmologystis And Symeoboccocus; ΙТ Eridein sequences (of desaturase, of Symethorystis and Symethococcus) Gene, minrobial ΙT M1: B101 (Biological study: roesA, for desaturase, of Dynechocyatic and Synechococous, nucleatide and incoded poptials saguinors of ΙT 156532-35-3, Delta 12 desaturas. Wymach: Tystis ECC: 714) 156532-36-4, Delta 12 desaturase (Symetheonorus ECOTOS). HI: PER (Properties) (umino acid sequence of: 103462-28-5 153462-29-6 103571<u>-</u>10-5 ΙT BL: BIOL (Biblogical study); PEP (Englerties) inublectide segmence of: L24 ANDWES 15 OF 19 HUMPLUS COPYRIGHT 1:17 ACS 1994:184.75 Do ument No. 120:184.18 A game and ding a phloroplast . hera. - fatty acid desaturase complements alterations in fatty acid desaturation and onloroplast copy number of the fad? mutant of Arabidopsis thalians. Iba, Moh; G.bson, Sue; Mishrucht, Takumi; Fure, Takuichi; Michimura, Mitsuo; Ar mdel, Vincent; Bugly, Sudanne; Someorbille, Chris (Pad. Sdi., Kyushu Univ., Fukubka, 81d, Japan). T. Bibl. Chem., 26%(3.), 34099-10% (English) 1995. CoDEN: JECHA3. ISSN: 7001-9055.

Mutations at the fad7 locus of A. thalian: (previously

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AB

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called tadD) cause decreased desatn. of dienoic
fatty acids in ohloroplas: lipids in plants grown
at elevated temps. This suggested that the Pad? locus encodes a
chloroplast .cmega.-3 desaturase that datalyzes the desath. of
lipid-linked 18:2 and 16:4 fatty acids. In order to clone the fad?
gene, it was first genetically mapped relative to the flanking RFLP
markers 4547 and 2433A on enromosome 3, and yeast artificial
chromosomes covering the locus were identified. A putative
desaturase cDNA clone that was isolated by low stringency
heterologous probing with a cDNA for an endoplasmic
reticulum-localized .omeg..-3 desaturase .fai3) hybridized to the
yeast artificial phromosomes and bould not be resolved from the locus by ESTAP mapping. Expression of the cDNA in transgenic fad7 \,
mutant plants resulted in restoration of will-type fatty
addin compon. and suppression of a previously obsd. effect of the fad7
{f mutation} in onlyroplast n . indicating genetle
complementation. The structural gene contained seven introns within
a boding sequence of 1888 base pairs, which encodes a 446-amino acid
polypeptide of 51,172 daltons. The N-terminal region of the fad7
game product contained a monsensus chloroplast transit peptide.
Except for the N-terminal domain, the deduced amino acid sequence of
the fact gene product had high homol, to the fact gene product,
indicating that fad7 encodes an .omega.-3 desaturase and that the
two genes arcse from a common ancestral gene. There was no apparent
effect of growth temp. on the steady-state levels of fad7 mRNA in
wild-type plants.
3-3 (Biochemical Genetics
Swatian pross-reference(s : 7, 11
fatty acid desaturase gener sequence
Anabidopsis; mapping sequence gene fact Arabidopsis
Arabidopsis thaliana
   (fatty acid desaturase gene fad7
   of, isolation and sequence and mapping of
Chleroplast
   fatty acid desaturase of,
   Arabidopsis thaliana game for, isolation and sequence and mapping
Decayribonucleic acid sequences
   of fatty acid desaturase gene
   fad7, of Arabidopsis thaliana)
Protein sequences
   of fatty acid desaturase, of
   Arabidopsis thaliana)
Genetic mapping
   oof fatty desaturase gome fad7, on Arabidopsis thaliana
   chromosome il
Gene, plant
FL: BIOL (Biological study)
   fad7, for fatty acid desaturase,
   of Arabidopsis thaliana, isolation and sequence and mapping of)
Chromosome
   Arabicopsis thaliana :, fatty acid
 desaturase gene fau7 mapping)
Teptides, biological studies
EL: BIOL Biological study)
    transit, in fatty acid desaturase,
   of Arabidopsis thaliana
149955-97-5, .omega.-3-Fatty acid
desaturase (Arabidopsis thaliana clone g4)
FL: PRP (Properties)
    amino asid sequence of)
153602-91-4, Ger.Bank $66769
LL: PEP (Properties)
   inucleatide sequence of and mapping of:
                       KATHLEEN FULLER BT/LIBRARY 308-4290
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L24 AMSWER 16 OF 19 HCAPLUS COPYRIGHT 1997 ACS
1994:47043 Decament No. 125:47 4\% Claning of higher plant .cmega.-3
                              Yaday, Narendra
     fatty acid desaturases.
     3.; Wierzbicki, Anna; Aegerter, Mary; Caster, Cheryl S.; Ferez-Grau,
     Duis; Finney, Anthony I.; Hitz, William D.; Bootn, J. Russell, Jr.; Bohweiger, Bruce; et al. [Exp. Stn., E. I. duPont de Nemburs and
     Co., Wilmington, DE, 198x0-0402, USA). Plant Physiol., 103(2), 467-76 (English) 1993. OCHN: PLPHAY. ISSN: 00°2-1889.
AΒ
     Arabidopsis thaliana T-DMA 'mansformants were screened for
     mutations affecting seed fatty acid compn. A mutant
     line was found with request levels of linolenic acid (18:3) due to a
     T-DMA insertion. Genomic DMA flanking the T-DMA insortion was used
     to obtain an Arabidopsis oDNA that encodes a polypeptide identified
     as a microsomal .omega.-  fatty acid
     desaturase by its complementation of the mutation.
     Anal, of light content in transgenic tissues demonstrated that this
     enzyme is limiting for 18:3 prodn. in Arabidopsis seeds and parrot
     nairy rocts. This CDMA was ared to isolate a related Arabidopsis
     cDNA, whise mSNA is accumulated to a much higher level in lesf
     tissue relative to root tissue. This related cDMA encodes a protein
     that is a nomelog of the mississmal desaturase but has an N-terminal
     entension deduced to be a transit peptide, and its gene maps to a
     position consistent with that of the Arabidopsis fadD locus, which
     controls plasted .cmeda.-% devath. These Arabidopsis cDNAs were
     used as hybridization probet to isolate cDNAs encoding homologous
     proteins from developing seeds of scybean and rapeseed. The high
     degree of sequence similarity between these sequences suggests that
     the .:mega.-3 desaturase: use a common enzyme mechanism.
     3-3 (Bischemical Genetics)
     Seption pross-reference(s): 7, 11
     sequence plant fatty acid desaturase
     pene; Arabidopsis fatty acid desaturase
     yene fact; soymean fatty acid desaturase
     gene fadD; rapeseed fatty acid
     desaturase game facili
ŢΨ
     G÷ne, plant
     RL: RICL (Biological study)
         fact, for fatty acid desaturase of
        Arabidopsis and scybear, and rapeseed, sequence of)
ΙT
     Arabidipsis thaliana
     Brazeles napus
     និក្សាធនា
        fatty acid desaturases of
        migrosomes and chloroplast of, sequence of genes for)
         Hintlenic acid level: in Arabidopsis thaliana, bloning of
      fatty acid desaturase gene affecting)
IT
     Epotein sequences
        of fatty acid desaturase, of
        Polybean and rapesedd and Arabidopsis midrosom- and chloroplast)
ΙT
     Decomprischusteid asid sequences
          implementary, for fatty acid
      desaturase, of soybean and rapeseed and Arabidopsis
        minrosome and onlonoplist)
IT
     Bene, plant
     RL: BIOL (Biological study)
         factD, for fatty acid desaturase of
        Arabidopsis and soybear, and rapeseed chloroplast, sequence of)
ΙΤ
     463-40-1, Linolenia acid
     EL: PEP (Properties)
        (Arabidopsis thaliana Leeds with reduced levels of, bloning of
      fatty acid desaturase gene dausing)
ΙΤ
     149955-96-4, .omega.-5 Fatty acid
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desaturase (Arabidopsis thaliana clone CFl gene fad3)
     149955-97-5, .omega.-? Fatty acid
     desaturase (Arabidopsis thaliana chloroplast clone CFD gene
     fadD precursor) 149956-00-3, .omega.-3 Fatty
     acid desaturase (Glycine max clone GM3 gene fad3)
     149956-01-4, .omega.-? Fatty acid
     desaturase (Glyrine max biloroplast bline GMD gene facD)
     152208-01-0, .omega.-: Fatty acid
     desaturase (Brassica mapu: chloroplast clone BND gene :adD
     precursor) 152208-02-1, .omega.-3 Fatty
     acid desaturase (Brassica napus clone BM2 gene
     i be i
     FL: PEP (Properties)
        (amino acid sequence of)
                                                 149958-93-1 151497-59-5
     149995-89-5
                   149955-90-8
                                   149955-92-0
     151497-60-3
     FL: BIOL (Biological study); PEP (Properties)
        (nucleotide sequence ci)
L24 ANSWER 17 OF 19 HCAPLUS COPYRIGHT 1997 ACS
1993:318789 Document No. 119:218628 Map-based cloning of a gene
     controlling omega-F fatty acid
     desaturation in Arabidopsis. Arondel, Windent; Lemieum,
     Hertrand; Hwang, Inhwan; Cibson, Sue; Goodman, Roward M.;
     Somerville, Chris R. (Plant Res. Lab., Michigan State Univ., East
Landing, MI, 48824-1812, USA). Science (Washington, D. C., 1885-),
     258(103(), 1353-5 (English: 1990. | CODEM: SCIEAS. | ISSN: 0036-8075.
AΒ
    A gone from the flowering plant Arabidopsis thaliana that encodes an
     .pmeda.B desaturase was cloned on the basis of the genetic map
     position of a mutation affecting membrane and storage
     liptd fatty soid compn. Yeast artificial chromesomes covering the
     genetic locus were identified and used to probe a Brassica napus seed rONA library. A B. napus rONA clone for the desaturase was
     identified and introduced into roots of both wild-type and mutant A. thaliana plants by Ti plasmid-mediated
     transformation. Transgeburg tissues of both mutant and
     wild-type plants had significantly increased amts. of the
     fatty acid produced by this desaturase.
     3-3 (Biochemical Genetics,
     Geotion pross-reference(s : ), 11
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     cmeda? desaturase gene mapping Arabikobsis; cDNA omega: desaturase
     sequence cloning Brassics
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     Arabidopsis thalians
        tgerme fad3 fir .imega.s linkleate desaturase of, mapping of)
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     Genetic mapping
        (of gene faul for .omega.) linoleste desaturase, of Arabidopsis
        thaliana)
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        (of .omega.: lincleate desertrase, of Brassida nabus)
TT
        (transformation of, of Arabixopsis thaliana, by .omega.3
        linoleate desaturase DDMA of Brassica napus)
ΙT
     Bra wida napus
        7. gmeda. Flincheste desaturate cDNA of, sequence and cloning in
        Arabidopsis thaliana off
IΤ
     Gene, plant
     RL: BIQL (Biological stury)
        (fadf, for .omega.3 limpleate desaturage, of Arabidopsis
        thaliana, mapping and complementation of)
     Deoxyribohucleic adid sequences
          complementary, for .omega.U linbleate desaturase, of Brassica
        mapus)
ΙT
     Transformation, denetic
        (transgenosis, of Arabidopsis thaliana roots, by .omega.3
                             KATHLEEN FULLER BT/LIBRARY 308-4290
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linoleate desaturase cDNA of Brassica napus)
     Chromosome
         Arabidopsis thaliana 2, gene fad? for .omega.3 linoleate
         desaturase mapping on)
     148814-49-7
ΙT
     RL: BAC (Biological activity or effector, except adverse); PRF
     (Properties); BIOL (Bibliogical study)
        (amino adia sequende of, dimplete)
     27213-43-6
     EL: FORM (Formation, nonpreparative)
        -formation of, by transgenic Arabidopsis thaliana expressing
        Brassica napus .omega.? linoleate desaturase cDNA)
     143/10-76-3, GenBank L01418
ΙT
     BL: BIOL (Biological study); ERP (Properties)
        inuglestide sequence of,
L24 ANOWER 15 OF 15 HOAPLYS CORYRIGHT 1997 ACS
1993: 653:676 Document No. 119:188876 Fatty acid
     desaturase genes from plants and their use in altering fatty
     adri composition of plant pils. Browse, John; Grau, Luis Perez;
Finney, Anthony J.; Pierce, John W., Jr.; Wierzbicki, Anna M.;
     Yaday, Marendra S. (db. Bont de Nemburs, E. I., and Co., USA). PCT
     Int. Appl. WO 9311245 Al 940610, 167 pp. DESIGNATED STATES: W: AU,
     BR, CA, TP, BU, CA, US; FW: AI, BE, CH, DE, DK, ES, BR, GB, GB, IE,
     IT, LU, MI, NL, FI, SE. (English . CODEN: PIXXD2. APPLICATION: WO HE-USIN: 44 921203. PRIORITY: UN 31-814289 911214.
     Elastid and microsomal delta-15 desaturase cDNAs
AВ
      f Arabidopsis thalians, Brassida hapus, and Glydine max are cloned
     and seepenhed. The effect on 13:2 and 18:3 content of expression of
     antisens» delta-15 desaturase dDWA in B. napus
     and G. saw was examd. Use of the cloned cDNA for RFLP anal. and
     plant breeding was explored.
IC
     1004 01/10015-53
     TOD CIENCIS-88; G118901-10; G180001-68
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     3-3 (Bit Themical Genetics)
     Section Pross-reference(s): 11, 17
     fatty acid desaturase offia plant
ST
     sequence; Arabidopsis deltali desaturase oDNA sequence; Brassica
     deltal5 desaturase cDNA sequence; Glycine deltal5 desaturase cDNA
     sequence; cil glyseridic plant unsato fatty acid; EFLP plant
     rrending desaturase cDNA
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     Flant breeding and selection
         RELF anal. in, plant .DELTA.-15
      fatty acid/glyperblip-id desaturase
        ∪DNA :br)
     Gene, plant
ΙT
     Rh: BIOh (Billogical study)
        if or .DELTA.-15 fatty acid
         gly-erolipid desaturase of Arabidopsis thaliana and
        Brasbids hapus and Blydine max
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     Eromein dequences
        http://doi.org/10.1001/10.1001/2016
         gly meralipia desaturase of Arabidopsis thuliana and
        Brossins happe and Hlydine max-
     Flant
        toil-producing, alteration of Linolenic acid content of
        ransgenic, bloming of plant .DELTA.-15
        Hesahurase oDNA in relation to)
     Arabid:psis thaliana
     Bransica napus
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      acid glycerolipid desaturase cDNA empression
        in, fir alteration of linologic scid content of oil)
     Par. and Glymeridic bils
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     EL: BIDL (Biclogical study)
        swith altered linelenic adit content, transgenic plants
        producing, cloning of plant .DELTA.-15 desaturage cDNA in relation to:
     Deckyricanu sledo adia sequende
         openplementary, for .DELTA.-15 fatty
      acid/glyperalipid desaturase of Arabidopaia
        thalians and Brassica mapus and Glycine max)
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     Genetic polymorphism
        Trestriction fragment length, of plant genomes, plant
      .DELTA.-15 fatty acid
         glysemalipid desaturase aSMA for anal. of:
ΙT
     149955-96-4, .DELTA.-15 Decaturage
     Anabitopsis thaliana of me pCP3: 149955-97-5,
     .DELTA.-15 Fatty acid
     desaturase (Arakidopsis inaliana ol me pACEZ-I plastid)
     149955-98-6, .DELTA.-15 Glycerolipia
     desaturase (Prassica napus clone pBMSP3-2 microsomal)
     149955-99-7, .DELTA.-15 Glycerolipic
     desaturase (Brassica napus clone pBMSFd-2 plastid)
     149956-00-3, .DELTA.-15 Desaturase
     (Glycine man clone pKF1 microsomal) 149956-01-4,
     .DELTA.-15 Desaturase (Gly-line max dine
     pSF()-1183-wp plastid) 149956-02-5, .DELTA.-
     15 Desaturase fragment (Sea mays offene pECREO.
     149956-03-6, .DELTA.-15 Decaturage
     fracment (Arabidopsis theleana clone pFack-2 plastid)
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        camino asid sequence - f
     14 (15-8 -5, DMR (Arabid pris thali ma clone pCF3 .DELTA.-
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     15 desaturase oDNA and flanks) 14 (905-90-8, DNA
     (Arabidogsis thaliana of he pACEU-2 plastic fatty
     acid .DELTA.-15 desaturase
     cDUA and flanks) 149955-41-3, DNA (Prassica napus clone pBNSFS-2 microsomal .DELTA.-15 glyperolipid desaturase cDUA and flanks) 149955-42-1, DNA (Glycine max clone pXF)
     microsemal .DELTA.-15 departurase cDNA and
     flanks) 149955-98-1, DNA (Grycine max clone pSFD-118bwp plastid
     .DELTA.-15 desaturase cDNA and flanks)
     14:05-94-2, DWA (Zea mays clone pP %40 .DELTA.-15 decaturate cDMA) = 14995 - 00-3, DWA (Arabidoptis thaliana clone
     pFacemes plastic .DELTA.-15 desaturace cDNA)
     EL: BIOL (Exclipidal study,; PER (Properties)
         inuclection sequence if, use in RFWP anal. and in transgenic
        plants for alteration of farty and content of oils of)
     46 -46-1, Linglania acid
ΙT
     P.I.: PP.P (Properties)
          tran.denif plants prograins oil. with altered levels of, cloning
        + f plant .DELTA.-15 desaturase dDNA in
        relation to:
L24 ANIWER 1: OF 19 HOAFLUS COPYRIGHT 1997 ACS
1991:18074 Document No. 114:1-574 The OLE1 gene of Saccharomyces
     derevisiae en odes the .DELTA. Fatty acid
     desaturase and can be functionally replaced by the rat
     stearcyl-CoA desaturase jene. Stukey, Joseph E.; McDonough,
     Virginia M.; Martin, Charles E. (Nelson Biol. Lab., Rutgers, State
                             HATHLEEN FULLER BT/LIBRARY 308-4290
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Univ., Picsataway, NJ, (9355-1059, USA). J. Biol. Chem., 265(33),
     20144-0 (English) 1990. CODEN: JBCHA3. ISSN: 0021-0253.
     Strains of S. derevisiae bearing the olel mutation are
AB
     sefeective in unsatd. Satty acid (UFA) synthesis and require UFAs for
     growth. A previously isolated yeast menomic fragment complementing
     the old! mutation was sequenced and dotd, to encode the
     .DELTA.9 fatty acid desaturase encyme
     by companison of primary amin: acid sequence to the rat liver
     she royl-CoA desaturake. The OLET structural gene encodes a protein
     of 510 artino acids (2.4 hydrophobic) having an approx. mol. mass of
     10.4 kDa. A 257-amino acid internal region of the yeast open.
     reading frame aligns with and shows Fill Identity and 60% similarity
     to the rat liver stearcyl-CoA desaturise protein. This comparison
     disclosed 3 short regions of high convertive amino Abid identity
     \ell \cdot 70 ) including one 11 of 12 perfect residue match. The predicted
     yeast enzyme contains .gtpreg.4 potential membrane-spaniing regions
     and several enorter hydrophobic regions that align exactly with
     simular sequences in the rat liver protein. An olel sene-disrupted
     yeart struin was transformed with a yeast-rat chimeric wene
     consisting of the promoter region and M-terminal 27 dodons of OLE1
     fused to the rat desaturase coding se pience. Pusion gene
     transformants displayed near equiv. growth rates and modest lipid
     compa. changes relative to wild-type yeast control implying a
     significant conservation of .DELTA.9 desarrase tertiary structure
     and efficient interaction between the rat desaturase and yeast
     ggs - throme bi.
     9-3 (Brownems hal Genetics)
CC
     Seption oross-reference(s): 7
ST
     fatty acid desaturase gene sequence
     Sadinaromydes; geno OhEl requence Sad thanomydes
     Sad marchydes derevisiae
        (fatty acid desaturase gene GLE1
         f, nucleatide and enorded peptide sequences of)
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     Endiplasmic reticulum
        (fatty acid desaturase insertion
        into call membrane of, of Saccharomyce. cerevisiae)
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        fof fatty acid desaturase, of
     Japoharomynes ceremisiae, complete
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        tof transformed Sauchardmydes derevisiae contq. fatty
      acid desaturase dene
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        estearsyl CoA desaturase gené in, of yeast della contq.
      mutant fatty acid desaturase
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         stear yl CcA deserurase gene of, in complementation of
        Machinal omynes deperisiae contg. mutant fatty
      acid desaturase denel
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      fatty acid desaturase gene)
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         OLE1, for fatty acid desaturase,
        of Sacchar myces cerevisiae, nucleotide and encoded peptide
        …equences ∪f)
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    131198-85-1
    FL: FFF (Properties)
        famino acid sequence of)
ΤT
     3014-34-0, .[ELTA.3 Fatty acid
     desaturase
     FL: FFF (Properties)
        gene for, of Maccharomyces cerevisiae, structure and
        complementation anal. of)
     191198-68-6, Deckyribonucleid adid (Sadcharomydes derevisiae gene
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     [Nucleotide sequence of) 
57-11-3, Fatty acid 16:0, biological studies 57-11-4, Octadecanoic
    acid, michogical studies 112-80-1, %-Octadecenoic acid (Z)-,
    kiological studies 373-43-9 544-63-8, Tetradecanoic acid,
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      acid desaturase dere ;
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    Desaturase, oleoyl coenzyme A (Petroselimum crispum clone ELI12)

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          181 CLEMBETTUR REPONIETYY ELLDINPROFU INWLTTLLIG FRLYIMENVO
          HOL GHRYERWISH YOPHSPLYSO REFRELLYSD LALLAVLYDD YQDVDANGFA
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      Desaturase, ratty acid .omega.b- Petroselinum crispum clone 15-1) %I) (A INTEX DAME
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      196217-80-8 REGISTRY
      384-721-Desaturase, bleate (Corvins aveliana clone I) (9CI) (CA
      INDEX NAME:
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                        101 SUNGSEDERDE VEVERERSEN ENFSKYFILIF PGEVETSLIT LALGWELYLA
        151 MUSSERPYOR FACHYDDYGP LYCHERROGI PUDDAGUFAT TYULYYAAMS
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     196217-78-4 REGISTET
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      becaturase, - Leoy. Lecithar (Erossica napus cuenc Q50 : isseenzyme F)
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        151 LERDEYFYPK KKSDIKWYGK YHNNPLGRIY MUTVOFTLGW PLYLAFNYSG
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        RSA SIMUFYGUPL LIUUGFLMLI IYLÇHTHPSI PHUDSSEWDW LEGALATUDE
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126 ANUMER 6 OF 10 REGISTRY COPYRIGHT 1097 ACS EM / 192889-79-5 REGISTRY
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301 DYGILNKVFH NITDTHVAHH PESTMPHYHA MEATKAIKPI LGEYYOFDST
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       331 POVKAMWREA KECHYVEPOR OGEREGVEWY NUKL
HITS AT: 1 (5-10), 141-141, 31(-33)
MF Unspecified
CI
    MAH
17.
    CI
     STN Files:
                 CA, CAPLUS
                1 REFERENCES IN FILE TA +1967 TO DATE)
1 REFERENCES IN FILE SAPLUS (1907 TO DATE)
           1: 127:135024
REFERENCE
1.6 ANSWER 5 OF MG FROIDTEN COPYRIGHT 1997 ACS FIT \frac{1}{3} 192889-75-1 REGISTRY
    Desaturase, olegyliscithir. (Brossisa napur strain Westar isoenzyme
     D) (9C1, (CA THEEN NAME)
     EROTEIN DEGUENCE
:QL 384
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                ----- location ----- description
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uncommon.
                Аза−6Э
        1 MGAGGEMOVE PROMISERED INTERPORTER FINGELMMAI PRECEMPAGE
        SI AMPSYLIMDI IMACCEYYKA TOYFELLEHE LSYFAWELYW ACQGCVLTGV
       101 WVIAHEOGHE ARMEDOWNDE TUGLIFHSEL LVFYFSWEYS HREHHENTOS
       151 LERDEVENPH PRODUKWYCH YDDUPLGETY MDYYCETDGW PLYLAFDYSG
       301 EPYDGGFFCE FHENAPIYUD FEELQIVISD AGILAVCYGL FEYAAGQGVA
       LEI SINGEYGUPA LUNGGINIA TYLOHTHESA PHYDSSEWLW FEGALAIVDE
ECI DYGILHBUFH NITDIHVAHH EFUTMPHYHA MEATRAINFI LGEYYOFDGT
                            :: =:=::=
       :51 PVVKAMWEEA HECTIVEPTE (GHEEGYEWY DDEL
HITS AT: 140-100, 141-140, 016-00
    Unspecified
( · :
    MAII
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     STN Files:
                 CA, CAFILLE
                1 ARPERENCES IN FILE (A. 1967 C. DATE)
                1 REFERENCES IN FILE CAPACE (15-7 TO TATE)
HEFERENCE 1: 1.0:131044
126 ANSWER - OF A FROITTEN COSTRUCET 1897 ACC
     186208-06-0 REGISTER
     Devaturase, .DELTA. - Fatty acros P.chia angusta) (901) - (CA INDEX
     NAJED
F.:
     PROTEIN SEQUENCE
                                                                               1 (
SQL 451
         1 MOTESMITOUT AMELORDOUA MMIMARDRELE TRULKQUEETS EQRWIWENWE
SEQ
        51 RHINWINEIL VLAVERAGII SYRWVENKUR TEUTAVILYO FOGISITAGY
       101 HERMARPAYD CHUPYKIFFA DPOASAYEGS IKEWGEQHEV HERYIDIPRI
       151 PYDAKROFWY SHMOWNLINP NERYKARADI SELLODWAVE VQHRHYLLLIM
       201 VUMAFREPAU REHYDENDEW GOFFYAGILE AVTIQQATEC VESLAHWIGE
       231 OPFDOMETRE DEVICALITY GESTHNEHE FEIDYEMALK WYGYDETKYV
       301 IYLLSHI'JLA YULHURSONA IDQ ILQQQQ HHUDEMBARL NWGPQLCELP
       351 VWDKSTFFER AREQUEDIVII SGIMHDCANF LIBERGEQAL LEISFGEDAT
       401 MAFNGG YAH SNAAHNLLAT MRYAVINDOG ANGDTFDAGL RYLASKENKK
                            HATHLEEN FULLER BT/LIBRARY 308-4290
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451 E
HITS AT: 138-142, 275-279
MF Unspecified
    147411
CI
: F.
    +17x
     ∷T∷ Fil∈s:
                  CA, CAPLUS, TOXLIT
                1 REPERENCES IN FILE CA (1:007 TO DATE)
1 REPERENCES IN FILE CAPLUS (1:007 TO DATE)
REFERENCE
            1: 116:1139)1
126 ANGWER 11 OF WO REGISTRY COPYRIGHT 199" ACC
EN
     180583-92-0 REGISTRY
. . .
     Desaturase, lincleato (Boragi officinali) (OII) (CA INDEX NAME)
     PROTEIN SEQUENCE
.`QE
    448
         1 MAAQEKKULI SDEDENEDKE EDIMICIQOK AYOVEDWUKI HPOGSFPLKS
.EQ
         31 LAGOMUTDAF VAFHFASTWK MIDREFTGYY LKIYSUSEUS KDYRKLYFRE
       101 SEMGLYDEKG HIMFATLOFI AMLFANSVYG VLECEGVLUH LESGOLMGFL
       191 WIQSGWIGHD AGHYMVVCDS FLEMFENGIFA ADGLEGIBIG WWRWNHDAHH
       LGI IAGNGLEYDE DUGYYPFINY SCHEPGSLIC HYYEKKLIFD SLBEPFYSYQ
USI HWIFYPIMCA ARLINYYQSU IMLLIFRNYC YRAGELLGGI VESIWYFILW
       POI SCLPWOLKI KEVIASLOVI GMOOVOFSIN HESSSYYVGK PKONNWELKO
PSI TOGTADIO S FWEDWERGGS OPOIEHHLED KHELCULRKI SPYVIELCKK
       411 HMLPYDYADE CERNEMINET LENTALQARD ITEPSPERIN WEALHTHG
HITS AT: 159-163, 136-100
    Unspecifical
. . I
     MM
. F.
     CT_{\Lambda}
     UTD Files: CA, CARLUS, TOXLIT, USPATFULL
               . PREERBOOKS IN FILE CA (1967 T) DATE
                . REFERENCES IN FILE CAPLUS (1907 TO DATE)
REFERENCE
           1: 000:289090
           2: 11:1614 (
REFERENCE
126 ANGWER 11 OF TO REGISTED COPYRIGHT 1997 ACC
     175960-67-5 EEGISTEN
     omidase, lather terel (Arabidopsis thaliana come pFL6101) 901) (CA
     INLEX NAME.
     PROTEIN SEQUENCE
SQL 281
         1 MAARMAYING EVDETSEYNE IVINTHIMEAN IMPELHEENÇ TWIRNYLAGT
SEQ
         SI LLYTISGENW CEYIYYERIM VYLEKDAIFT IKAMELÇMEV AMRAMPWYTL
       101 LETVIENDIE EGWIFCFASI GEFOWILYD YLAIYLVFUE FGLYWMHEEL
       151 HDIKPLYKYL HATHHIYNKO NYLEFFAGLA FHEYDGILOA VPHVIALFIV
                        .:(1 FIRFTTHIGL LFMEAIWAAN INDCHIGNIW PYNGAGYRTI HRTTYKENYG
       251 HYTIMHEWAF GOLKIPLLES DINKDOFKFA E
HITS AT: 147-151, 161-165, 305-207, 222-326, 239-232, 247-251
115
     Unspecified
ЭΙ
     IIAN
SR
     CA
LC
     STN Files:
                  GA, CAPLUS, TOXLUT
                1 REFERENCES IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (19.7 TO DATE)
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. REFERENCE 1: 124:309005
 IL16 ALISWER 12 OF 26 EMPLISTRY COPYRIGHT 1997 ACS
 EN 168613-13-6 REGILTEY
  Desaturase, a vylovennyme A (Anacystis midulans strain ED-SPc
      reduced) (PCI) (CA INDEX NAME;
  OTHER MAMES:
  Disaturase, anyl dremnyme A (Symethococour strain PCC 6301)
  FO PROTEIN SEQUENCE
 30L 278
          1 MTDAIRPKLA FRWPTALEMY AIHIGALLAF LPANTHWPAY GVMVALTYIT
 ЗEQ
         51 GCFGITLGWH FLISHESFEV ERWLEYYLVE CGTLAMDHGP IEWIGLHRHH
        101 HERSTON DE HOUNESFLWS EFLWEITE ARTEVORFTE DIAGDETYEF
        151 FREYFFOUDY LLOVILYAWG EAWVORGWSF VVWGIFARLV WYTHVIWLVN
        . 51 GATHEFOTES HEUGDOSTNO WWYALLAFGE GWHNNHHAYO YSAFHOLDWW
        .51 EPDLTWHILD CHRUNGLARK INVASPIN
 HITS AT: ) = 132, 233-23
 MF Unspecificed
 CI
     MAD
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      C_{IA}
      STU Files: CA, CALLYS
                1 PEFFERNCES IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1905 TO DATE)
 REFERENCE
           186 ANSWER 18 OF THE REGISTEN COFFEIGHT 1997 ACC
      163961-98-6 FEGURIFY
 CII
      Decatumate, :atty asic .cmega.6- Arabidopsis thaliana gene fad6)
      (BOI) (CA INDEM NAME)
 £,'',
      PROTEIN SEQUENCE
 31L 418
 SEQ
          1 MASSIANCIF AFTGEROOLE ENPELAASSA ENVEGYYAVE PIDLIINGET
         51 HESEFCUAFY KEFIGÜIKAN AARVAPPSAD SAEDREQLAE SYGERÇIGED
        101 GPENVILKOT NOCLPREVEE HOLKALKSV LIGVIOYTIG DEMIARGEWY
        #31 LIPLAWAWIG TAITGEFUIG HICAHRSESK NEUVERIVGT LARLPHUYEY
                                  := = :: ::::=:
        .01 ROWRERULAH HARTURLMHD TAMOPMPERE FROSPUMRKA ITEGYOPTER
         31 WEGIAHWIDW HEDERFFRAG EVNEVKISLA OVFAFRAVOW PLEVYKVGIL
         -01 GWYFFWIIGW IGYHFWMCTF TMYHHTAPHI PFEFADEWNA AQAQLNGIVH
                                      +51 CDYPSWIEIL CHIINWEIPH HISPEIPSYN LEAAHFSIGE NWGKYINLAT
                             401 WIWELMETTIN TUCHUYDH
 HITS AT: 171-171, 200-.11, 325-329, 367-371
 M_{F}
      The pecified
      ML
      C_L
      STE Files:
                 CA, CALLUS
                  EMPERED ES IN FILE CA (1967 TO DATE)
                 : REFERENCES IN FILE CAPLUS (1957 (1) DATE)
 REFERENCE
           1: 1. :28504
 LL6 ANDWER 14 OF the REGISTRY COPYRIGHT 1997 ACC
 N.3
      161027-24-3 EMGISTEY
      D-saturase, facty acid .DELTA.15- (Synephocy.tis sp. PCC 6603 clone
      pbluescript/6.u-kbp gene desB] (9CI) (CA INDEX NAME
                            KATHLEEN FULLER BT/LIBEARY 303-4290
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Typ-

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.OTHER NAMES:
     .omega.? Desaturase (Synechocystis sp. 200 6203 clone
      pRimesoript/6.6-kbp game desE.
     GenBank Dulkla-derived protein GI 1601333
     Pridein (Symethic syntia strain, PCC 0903 blone
      os1068/ m/ it is the first +23/ me0391 open reading frame s111441
      re moed:
      PROTEIN SERSENCE
F'. :
SQL
     359
31.0
          I MELETAGEOT KUPYEKTEEL EFTLOELENA IPAD FEBSV VRSLGYFFLD
         OF THE LEAGUESTAL AVAILABENCETY PREMITIGATE EMPLICACIONE CHESSESKEY
                                                         101 TLMIWIGHLS BTPIGAPTHG WRISHRTHHA NTGNIDIDES WYPYSEOKYN
        151 QMANYERELE FYLPHIAYPI YLFEESYMEÇ GSHFMPGSPL FEPDEKAAVL
        201 TETFALAREN FELGETINGE ONLETIMETN APPLYEVYMI OLVIFLHETE
        161 DULPWYEGDO WYFLEGALST IDEOYGFINE ERHDIGIEVA HELFSIMPRY
        301 KURRATEATH FILGEYYRYS DEPIMQASEK SYWACHEVEN QGSEVYYQSE
        F51 UNGGTQEFF
HITS AT: 24-44, 1.5-1.9, 284-292
MF
     Unspection!
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     MAII
T.
     C_{T_1}
                  CA, CAPLIS, TOMEST
FEFERIOLE IN FILE CA (1967 TO DATE)
      2771 Fi. a:
                 I REPERENCES IN FILE CAPOUS (1907 TO DATE)
FAFEFENCE 1: 1.4:70 %1
PREERINGE .: 1.1:1.484.
 106 ANSWER IS OF BUILDERING COPYRIGHT 1997 ACC
      158651-91-3 FAGISTRY
511
177
     Desaturase, farty acid .cmega.?- (Arakidopsis thaliana clone DES1
      plastic-arsoriated becommymet (9CI: CA INDEX NAME)
C"HEE NAMES:
      Deraturase, facty acud .cmeqa.3- (Arabidopsis thaliana gene fad8)
£1.
      PROTEIN SEQUEDRE
30L 435
          1 MARGOLIFOG FERMFREYRK HITSEACKER PTEKFNERLK ERSSLIMSEN
330
        11 GEYOFTEDWA LINATELTTL OSESELFTE FORGALEREN LADIRAAIER
101 HOWMFREWAR INTYUDELUAI VEGLAAVAAY ENEWLIWELY WEADGTMEWA
111 GEYOGH GOEDDEELN SVAGELIHUS ILVEYHOWEL SHETHHONHO
        U01 BYENLEAWHE LEEDIYKNLE SITOMERETI PEPMLAYEFY LWNESPOKQG
        UBI CHYREDODE FERRETMET OTACWTAMAA LINCONEMMG FIQMLKDYGI
        301 PYWIFYDWUD FYTYLHHHGE EDKLEWYROF EWLYLEGGLT TLDEDYGWIN
                              21. mr _2 (2010)
        301 NORHOGOTHY CHRUFFQUER YRINEATEAA KEUNGHYYRE FENSGRIPIR
        401 LIGSLIYUME ,OHFUSDIGD VYYYEADPEL NGOKT
HITS AT: 1 6-16 , 1 1 -19 1, 316-320, 359-363
      Unspecitie:
     MAN
ξ.,
     GA
LC
      STN Files:
                    TILIKOT, RULISKI AK
                  EMPERATIONS IN FILE CA (1 (7 TO DATE)
                 5 EMPRENIOUS IN FILE CAPLUS (1997 TO DATE)
REFERENCE
            - 1: 125:26:∃1
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- REFERENCE
            2: 101:307500
 FEFERENCE 3: 1.11:.49101
 LOG ANSWER 16 OF 36 PROJETRY COPYRIGHT 1997 ACS
      158283-34-2 FEGINTEY
     - Desaturase, oleogi moennyme A (castor-oil plant clone pRF137C-42)
      reduced, BCI) WA INDEX MAME
 CTHEF NUMBES:
 TI delta.-II Fatty and desaturase (Richnus communis clone pEF197C-42)
      FROTEIN CEQUENCE
 Ξ,
 S(t)
     387
 SEO
          1 MGGCORMOTY FIGUNSERRG GSCHLEFARH THEPYTEGNE RFAIPPHOFE
          51 KGEMAGESNE AYNECLOPLS YSIATNEEPY ISOPLSYVAW LVYWLEQGQI
         101 DIGLWWIGHE OGHHAEREYQ LADDIVGLIV HSALLVEYES WKYSHERHIS
         131 NIGGERADEV FUPKSYUKIŞ WYGKYLNAPP GEVLTLAATL LLGWPLYLAF
        U01 MYSGREYDRE ACHYDEYGET ESBEERLOIY IADLGIFATT EVLYQATMAK
        .51 GLAWVMFLYG UPDDIVLGFU VMITYDQHTH PAIPRYGSSE WDWLRGAMUT
-01 MDRDYGULNK UPBNIADTEV ABHDFATVBH YHAMBATKAI KBIMGBYYRY
 -31 DGTHFYFALW REWRECLEVE EDECARTOGY FWYRNKY HITS AT: 1)3-11:, 14 -143, \times 13-32+
 MF Unuperafied
      N = 1
 34.
      \mathbb{C}\mathbb{A}
      STM Files:
                  CA, CALINIS
                 1 PEPERANCES IN PILE CA (1967 TO DATE)
1 REFERENCES IN PILE CAPLUS (1967 TO DATE)
 L. 6 ANIMER 17 OF 86 REGISTEN COPYRIGHT 1997 ACS
      158283-32-0 REGISTRY
      Desaturas, clery: nerryme A gastor-oil plant clone pFads1
      2.4-amin: wors fragment recurred) (PCI) (CA INDEX NAME)
 COHER MAMES:
     ..d-lta.-l. Patty and decaturase (Elizanus dommunis clone pEF2-10)
      FROTEIN SEGVENCE
 E(L 224
         1 WARRECORE APVOYCLIDO WGLILESCL LVOYFSWEES HERHENTGS
 3 : Q
          31 DEFESTIVER FRUITFWYSK YINNPPORIN TIAVTLEDGW FLYLAFNVSG
         101 RPYDEFACHY DEVOETYDDE BEIBIFISDA GVDAVTEGLY ÇLATAKGLAW
         180 MYCHYGUELL WURFEMLIT FLOHTHFALP HYDSSEWDWL EGALATVDED
        101 YGTIMEMEN TOOTOVAHHE ETHE
 HITS AT: 5-9, 41-45
 MF Unspecifica
      [v] [v]
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      ( )
      STN Files: CA, WHING
                 1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)
 EMFERENCE
             1: 121:11:546
 1.16 ALLWER 18 OF 36 RESIRIES COPYRIGHT 1997 ACS
      158283-30-8 FEGISTRY
      Denaturase, ole-yl cuenzyme A (corn clone pFad21 reduced) (9CI) (CA
      INDEX NAME)
 DIHER NAMES:
 CN .delta.-12 fatty acid desaturase (Zes may; clone pFad2#1)
                          HATHLEEN FULLER BT/LIBFARY 308-4290
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·FS
     PROTEIN SEQUENCE
SQL
     387
          1 MGABBEMTEK EREKOEOLAR ATGGAAMQES PVEKPPFTLG QIKKAIPPHC
SEQ
         51 FERSYLMOFO YUVHOLUIAA ALLYFALATI PAUPSPLRYA AWPLYWIAQG
        FOI CUCTONWILA HECCHHAFSI YSELDDWYGE VERGSENNDY ESWEYSHEEH
                        1.151553.2
        TOI HANTGSINEED EVEYPEREEA LEWITLYVYN NEWGEWUHIV VOLTLOWELY
        .01 LATMASGREY PREACREDRY GRIYMURERA QIFYSDAGVV AVAFGLYKLA
        . 54 AAR KWWENE UYAUPLLIVE AWLULITYLQ HTERSLERYD SSEWDWLEGA
        -01 LATMORIGGI LUBUFRUITI THVAHELFST MERYHAMEAT KAIRPILGDY
                                     =:::::: = :
        39-1 YHEDETEVAK ATWREAGEOL YVEDEDERGV EWYNYKD
HITS AT: 111-111, 14:-111, 241-126
MF
     Un pecifica
     MAJ
37.
     CL
     STE Files:
                   NA, CAELUS
F.( *
                 I REFERENCES IN FILE CA (1967 TO DATE)
                 DEFFERENCES IN FINE CALLUS (1969 TO DATE)
             1: 1:1:1:40
REFERENCE
1.6 ANSWER 13 OF 36 AMBISTRY COPYRIGHT 1937 ACS
Γ,
     158283-28-4 EEGICTRY
     Desatures, (legy) mercyne A % cykean oline pSFM-165F reduced) (MME) (A INDEM NAME)
OTHER NAMES:
     .omlta.-I. Forty acros desaturase. Glycine max clone pSFS-1(5K)
     FROTEIN SEGURNOR
. · · _
    379
          1 MOGRICANUL ANGGERFINE MENUFUFFTV GOLFKALFFH CFOESLLTEF
33.0
         51 SYNYYEN FA FIFTIATTYF HELKÇEFSDI AWELYWULOG CLLIGWWYLA
        101 HECCHEAFOF YOMUTOUVGL TIHUTLINEY ESMHISHERH HSNTGALDAD
        191 ENFMERENSK NAWEMFYIMD PLOFANSLIN TENDOWERYE AFRYGOREYD
        101 SPASHYHIYA FIYOMERELI IYYOFTALES YTYSIYEVAT EKGLYWLLCY
281 YGYPLLIUMG FIYTITYIQH THFALIHYDS SEWDWLFGAL ATMERIYGIL
        ROI NEVERHITET HUARRIESTI PRYRADEATN AIPPILGEYY QEDDTEFYKA
       FULL IMPERATE OUT AMELICATES GAZAZENEY
HITS AT: 101-10', 197-111, 911-15
    Unspecified
     M7.11
SE.
     C_{I}.
                  CAFIDS
(C)
     STN Files:
                1 PREFERENCES IN PINE CA (1967 TO DATE)
1 PREFERENCES IN PINE CAPLUS (1967 TO DATE)
EMPEREDUE 1: 1.1:.1+64+
5.16 ALLWER 30 OF 36 LEGISTRY COPYRIGHT 1997 ACS
     158283-26-2 FEGUSTRY
-N
     Denaturase, ole yl chembyme A -Brassica hupus cuone pCF. -165D
V_{ij}
     re buced, PCI
                      (CA INDEX NAME)
OTHER NAMES:
CN
     .d-Ita.-12 Fatty actionsaturas (Brassic: napus clone (CF2-165D)
F'.3
     PERCEIN SEQUENCE
SQL 383
SEQ
          1 MGAGGENING PESKESETON IKRVPCETPP FT GELEKAL PPACFYRSIP
         51 RSFSHLIWDI HIASCFYYVA TTYFPLLPNP LSYFAWELYW ACQGGVLTGV
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HATHLEEN FULLER BT/LIBEARY 308-4290

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101 WVIAHECGHA AFSDYDWLED TYGLIFHSEL LYPYFSWYYS HRRHHENTGS
       151 LERDEVEYER RSQUBSGTAS TOTTFGREVN LOUDETHOWE LYLAFNYSGE
       201 PYDGGFACHE HEMAPIYNIR BELGIYISDA GILAVOYGLL PYAAVQGVAS
       .61 MYCELRYPLD IYNGELYDIT YLQETHPSLP HYDSSEWIWL EGALATYDED
       FOI YOILNQIFHN ITOTHEANHL FOTHPHYRAM EATRAINEIL GBYYQFOGTE
       *51 VYKAHWREAK ECTYMERDFQ GERYGVFWYD DEL
HITS AT: 100-100, 141-110, 015-710
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    MA:
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    \mathbb{C}I_{\Delta}
     STN Files:
                 -CA, CAFINE
               A REFERENCED IN FILE CA (1947 TO DATE)
               1 REPERENCES IN FILE CAPLUS (1 400 TO DATE)
EFFERENCE.
           1: 1:1:...6640
126 ANIMER IN OF 36 REGISTRY COPYRIGHT 1907 ACS
    158283-24-0 REGISTRY
     Desaturise, leoyl roomby\pi \in \mathbb{A} Arabidophus thaliana clone p\theta2103
    reduced: ( **!) JUN INDEX MADE:
OTHER NAMES:
    ..delta.-12 Fatty said desaturas (Arabidoggis thaliana clone p92103)
    Ol-ate desambrace (Arabidopsis thaliana clone pF2a gene FAD2)
= 1
    PROTEIN SECTENCE
    383
        1 MCWGGEMENT TUDENSHIET THEMPORKED PONGOLFFAL EPHOFFREIS
310
        81 RUFSYLISDI ITACCEYYVA THYFSLLPQP LCYLAWELYW ACQGCYLTGI
       1(1 WITAHE) BHH APCINGWILD TYCLIFHSEL LITEYESWRYS HARHESWIGS
       131 DARDEMEYER QROALFWYGK YLDDELGRIN HDIVQEVLGW ELYLAFDYSG
       .(1 RPYDGFACHE FEMAFIYMER RELLIYLSDA GILAVOEGLY EYAAAQGMAS
       REI MICLYGUELL INVAFIVAIT YAQETHESIP EDIKSEWIWA EGALATYDED
       301 YGILLEVERN ITUTHVAREL ESTMEHYNAM BATKAIREIL GDYYQEDGTE
       351 WYMAMYPEAK ECTYVEPDFE GDFKGYYWYN DEE
HITS AT: 10-1 , 141-145, 515-11:
....
    Unspecifies
MAD
    CF
     STM Files:
                CA, CAFIUS
               . BEFFRENUES IN FIRE (A 1967 % DATE)
                PEFFERNORS IN FILE CAPLUS (1 + 7 T) DATE)
FEFERENCE
           .l: 1.1:726640
FEEEEW.F
           .d: 1 1: 1435.
186 ANIMER A. OF TO ERCHMINY COPYFIGHT 1947 ACS
     156532-36-4 REGISTEN
    Desaturale, length outhin (Type chocide a strain PCC 7102 gene desA
    resided (+11) (CA IMPER NAME
DITHER NAMES:
CD Desta Destarase Oynecho to Fus PCC7 (...)
F:
     PROTEIN BEGTENCE
SUL 347
         1 HIBVTYEPSA TILLEKHPNI KIKDILDILP KUYYEINPLK AWSRYLLSVA
SEO
        DI ATTIGOTALLA TARMYLLLEV WELTGTTLIG FRIIGHROGE EGESROWVN
       101 NLYSHLAFLP LIYPFHSWEI LHNHHHRYTN NMDEDNAWAP FYPELYDDSP
                                  -----
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151 AFIKAVYRAI RGYLWWLASY IHQLKLHFUW FAFEGYQREQ VRFSALFVII
       201 AGAIAFPUME YTLGVWGVVY EWIMPWLGYH FWMSTFFLYH HTVPEIPFSY
       201 EDKWNEATAQ LSUTVHCDYP KWIEVLCHDI MVHVPHHLST GIPSYNLEKA
      301 YASIMQUWGE YUYETMEUWE IMMAITEQOH UYUAEMYIS FAQHQKR
HITS AT: \xi_1 = 90, 1.22 - 1.0, 1.23 - 1.0
MF
   Unapecitie :
CI
    MAH
3P.
    CA
                 MA, MARLUI, TOXLIT
REFERENCES IN FILE CA (1:67 T) DATE
     STN File:
               I REFERENCES IN FILE CAPLUE (1907 TO DATE)
           1: 1. (:2 ( ;; 7
REFERENCE
REFERENCE 1:1:74:..
136 ANSWER 33 OF 38 REGISTRY COPYRIGHT 1997 ACS
    156532-35-3 REGISTRY
5.11
    Devaturase, - Lebylowdathin (Symechodystis strain POC 6714 gene desA
     reduced: CCI: (W. INCEX DAME)
CTHEE NAMES:
311 Delta 1. desaturase Symethopyetis PCC6714)
    ERFTEIN SEMURIOE
3QL 349
        1 MTATTETTE TETSSUPPRE INDEKDOOT KTIPKFOFEK KASKAWASVI.
        31 ITLGATALGY LGCCYLEWYC LEFTWOWTHT ALIGAETWCE DOGERSFARK
       101 EWANDER HI AFAPLIYEFH SWELLHDEHR LRINKSEVEN AM PWSVEAF
       181 (ASPAIUSIE VERSEGERWW TOWNFEWGLM HEFLEDERER DENKYFLSIA
       301 VUFTFAAVAF FALTITTOVW GFURFWIMIW LVYHEWMSTF TIVHETIFEI
       TELL REPREDENTA ABAGINGTVE COVERNVEUL CHUNVELEH ELSVAJESYN
                                                  -----
      HOLD BLANAMING TWOSFLYFRE FLWGLMQQUS GOCHLYLYDD GYRTESSLEC
HITS AT: (8.491, 118-15., 181-191
MF Unspecified
C. T
    MZH
    (A
<u>.</u> ( :
     STIL Files:
                 - W. CALLUI, TOKLIS
               DEFFERENCES IN FILE CA (1:67 T) DATE
               1 PEPERBURE IN FILE CAPLUS (1907 CO DATE)
FREEDOM 1: 101:74:00
100 ANGWER 14 OF OUR EMPIRIENT COPYRIGHT 1980 ACC
    152208-02-1 REGILTERY
    Desaturase, firty and tonogate- Brassica namus clone FNB gene fad3
                     jya inlem name,
    reduced PCT
CTHER NAMES:
    .cmoga.-3 :atty a www desaturase Brassica napus clone BNS gene fad3)
    PROTÉIN SEQUENCE
3QL 377
         1 MINAMBORIN ANGERFIGG AGERRIGIG FAGGERICKY EURLRINGYV
SEQ
        NI ABDIFANNAL AVÆANYFDSW ÉFWELYWAAQ OTEFWALFYL OHLOGHOSES
       101 DIFLENDAUG HIBEUFILMP YEGMRISHET ERONECHVEN DECWVELPER
                                        771 51 1 51 51 7:2
       151 DEFINISHING MIANTUPLPH LAYPLYLWER OF REGORDS FYSIFAPSE
       201 ENLIAT.TTC WSIMLATLVY LUFLVGPVLV LHUYGVLYII EVHWLDAVTY
       251 LHHHGHDOFIL PWYEGKEWSY LNGGLTTIDE DY IFINIEH DIGTHVIHHL
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- KATHLEEN FULLER BT. LILLARY 308-4290

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331 FPGIPHYHLV DATKSAKHVL GEYYREPKIS GAIPIHLVES LVASIKKDHY
       HI WETGOIVEY ETDPOLYMYA SOMEKIN
HITS AT: 3. -96, 103-138, 291-256, 195-299
MF Un.pecified
\Gamma
    1474.1
G_{\Lambda}
1,6
     STO Files: CA, CAPLUS, TOXLIT
                PEFERENCES IN FILE (A. 1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1907 TO DATE)
FFFERENCE 1: 121:47 45
1.6 ANIWER .E F -6 REGISTRY COFFIGHT 1997 ACS
     152208-01-0 REGISTEY
    Desaturase, :atty acid .omega.3- (Brassica napus chicroplast-encoded
     which BND sens faul precursor reduced: (BNI) (CA INDEX NAME)
OTHER MAMES:
     .cmega.-3 tatty adea decaturase (Brassica napus chloroplast clone
     Billy gener flact precinsor)
     SPOTĖIN SEJURNOS
.', L 329
. E0
        - 1 MOYOUERDAI URALAAGAAY LAMWINWRLY WOAQGIMEWA LEVLGHICGH
        EL GAESTIFFALN GUAGHLIESS ELVPYEGWET SHETERONEG HVENDESWHP
                                                111 MARKIYEMAD KETREFRETÜ ELMILAYPEY LWARSECKKG SHYHEDSDLE
111 LEKERNEVIT OTACWTAHAV LLYCLNEVMG PUÇMLKLYVI PYWINVMWLD
       TOT FOTYLHANGE EDELPWYRGE EWGYLRGGIT TEDROYCLIN NEHHOLGTHV
       Fil IHHLEPÇILE YHLMBATRAA KEMAGKYYEE POKSGELELH LLGILAKSIK
       POI EURPUSIEGO UUYYEADPNI YGEIKVTAE
HITS AT: 4\sqrt{-8}, 6.-80, \sqrt{06-111}, 240-253
MF
MI
    Ur.specifie i
     Fiz
     1.7
                  CA, CARLUS, TOXLIT
     STH Files:
                : PEFERENCES IN FILE NA .1967 TO DATE)
: PEFERENCES IN FILE NAPLUS (1967 TO DATE)
EFFERENCE 1: 1.7:47048
1.6 ADDWER . 6 F + REGISTER COPYRIGHT 1997 ACS
     149956-03-6 PEGISTEN
     Devaturase, fatty arid .DELTA.1 - Arabidopsis thaliana clone
     pPack=2 fragment resuced 901 (CA INDEX NAME)
OTHER DAMES:
     ..DENTA.-1) desaturase frugrent. Arabidopa.s thaliana clone pFadx-2
     migratid
     PROCEIN SEQUENCE
...L 156
         1 BUYYKAFTAN MALDVATPLI TEQUPSEEDR ERFDEGAPEP FNLADIFAAI
         I PHECWVENEW MUMIYVUEDV AIVEGLAAVA AYENNWILWP LYWFAQGIME
       101 WALFVLOHOC BHGSFSNDFF LNSVAGHLLH SSILVPYHGW RISHETHHQN
                   = := :=:
        151 HGEVEN
HITS AT: 108-112, 144-151
ilir.
     Unspecified
3:
     V(E, V)
Si.
LC
     STN Files: CA, CAPLUS, TOXLIT
                            KATHLEEN FULLER BT/LIBRARY 308-4290
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1 REFERENCES IN FILE CA +1 +67 TO DATE)

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1 FEFERENCES IN FILE CAPLUATE (1967 TO DATE)
            1: 119:153376
FEFEFENCE
1.26 ANSWER 27 OF 26 FEGISTRY COPYRIGHT 1947 ACS
     149956-02-5 REGISTEY
    Desaturase, fatty acid .DELTA.15- (corn clone pPCE20 fragment
     reduced (901) CA INDEX NAME:
THEE MAMES:
   .DELTA.-15 desaturase fragment (Zea maya close pPCR10)
    PROTEIN SEQUENCE
SQL 126
200
        1 HHOMHSHIER OLEWHFITER DYROLEPRIK ELHFTTEFEL LAFFVYLLYR
           51 SPOKLESHEL FOSDLESPHE ESDVM/STTC WCIMLAGLLA MACAFGPLQV
       101 LKMYGIEYLV EVHWEDLYTY LEHHGE
HITS AT: 1-P, 122-126
   Unspecified
    M^{\mu}N
    CI.
     SIN Files:
                 CA, CAPLUS, TOXIIT
                1 REFERENCES IN FIBE CA (1967 TO DATE)
                1 REFERENCES IN FINE CAPLUI (19.7 TO DATE
FAFERENCE
            1: 119:159976
136 ANSWER 25 OF 56 EEGISTRY COPYRIGHT 1947 ACS
     149956-01-4 REGISTEY
    Desaturase, fatty weld .DELTA.15- (soybear clone pSFD-118bwp
    reduced; .901) (GW INDEX NAME)
CTHER MAMES:
   .DELTA.-15 desaturase (Glycine max cuche pSFD-118bwp plastid)
     .cmega.-) fatty arid desaturase [Clycine hax chloroplast clone GMD
    dene fadili,
E 1
     PROTEIN SECTENCE
3.L 453
       1 MATWYHÇROG LRELARVIRE PRIGAALSUT BENEFILOTNE VVAGREFQPL
31 ROMWABENWG DEWSARLEVA PIEBEQHSUD DYTTIGTIGVER EKLEREFDRGA
101 PRPFNLADIE AAIRHEGUVE DRWRSMSYUU EDUIAUFGLA AAAAYLNNWL
SEO
       181 VWFLYWAAQG THEWALETIG HOOGHOSEJI DSFLNOVVGH LLESSILVEY
                                   =::::::::::====
       201 HGWRISHETH HOHHGHAPNI ESWHPDPERD FEDLDTVTEN DEFTAPFPLL
                 # 10 min() \d ((100))=
       361 AFFNYLESES EGETGSHEDE SSDLEVPNEE ROMITGTACW AAMLGLLVGL
       ECT GETWIGHTOLL KLYGVEYTTE VMWLDLVTYL HEHGHEDKLE WYRGHEWSYL
       581 RGGNTTLORD YOWINKINED IGTHVIHHLE PQIPHYENVE ATEAARPVEG
       4C1 KYYREPFESA APUPFHLIGE TIESFETDHE YSDTGDVVYY QTDSKINGSS
       451 KLE
HITS AT: 171-175, 207-214, ©1-335, 374--78
Mar
     Unspecified
C:
     MAN
S:
LC
     STN Files:
                  CA, CAPLUS, TOXLIT
               2 FEFERENCES IN FILE CA (1967 TO DATE)
                2 REFERENCES IN FILE CAPLUS (1947 TO DATE)
REFERENCE
            1: 120:47048
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. REFERENCE 2: 119:153:76
 126 ANOWER H9 OF 36 ENGISTEY COPYRIGHT 19:7 ACC
      149956-00-3 PEGISTRY
     Desaturase, fatty acid .DELTA.15- soybear daone pXF1 reduced) (9CI)
       (CA INDEX DAME)
 OTHER MAMES:
     ... LELTA. - 13 desaturase (Clycine max clone pXF1 microsomal)
     .cnuga.-3 fatty acid desaturase (Glyrin max clone GM3 gene fad3)
      FRATEIN DEWURDCE
 SOL
      380
          - 1 MYKTTYPTAY AANNGYQQKG SSEDEDESAP PEFKIAETFA STEPHCWVKN
          'I FWESLYYDE DVINIAALNA AAIHFDHWIL WLIYCFIOGT MEWALFNLGH
         1:1 [CCH33FODS FLINSIMONI LESSIIMFTH OWEISHFTHH QUEGHIERDE
             151 SWYELTERLY RILIDSMIRLE RETVERFILEY YPLYLESESP GEBOSHFNRY
         .01 SNOFFFCEEK GIAGSTICWA TMESLHIYLS FITSPLLVLK LYGIPYWIFV
         101 MULTEVIYLE HERHORNEW YEGKEMOYIE OGITTVIKIY GWIYNIHEDI
                      = 75=2 0000
         · 1 OTHVIHHLEE OTERVHIMEA TOAAKPMLOD TYKEELESAP LEEHLIKYLI
               1 .:: 12 12.2.7.7
 +31 QUMBQDHFV3 DAGDVVYYQT FSLLLEGQED
HITS AT: 10-194, 136-140, 161-265, 003-30
 MF Unabedified
 · . . .
      M.-..
      CA.
 3.1.
      STM File: CA, CARLOS, TOKIJT
                 . HEFERENCES IN FILE CA 1007 TO DATE:
J HEFERENCES IN FILE CAPEUR (1907 TO DATE:
 ERFERENCE 1: $20:47648
 BEFERENCE :: 100:15:376
 LL6 ANSWER OF 36 REGISTER COLYFIGHT 1997 ACS
     149955-99-7 REGISTAN
 EII
      Desaturase, fatty aris .DENTA.18- Brassica mapus clore pPNSFd-2
      C-terminal transfer requied: (901) CA INDEX NAME
 OTHER MAMES:
      -.BELTA.-15 d.yrerolipid (esaturase Frassica napus clone pBNSFd-2
      plation
      PROTEIN JEGURIOE
 SQL 404
          1 PMFEQSECSE EFELNSEMMA INVITENTIO SENSEPHEEE PHIQREDESA
          OF PPPENDAMER AND PRHOWNE DEWRENDY'N RELATIVENTA AGANYLINWL
         1 4 VWELYWIAGG IMFWALETLG HECCHOOFID DEALNOVER LLEGSILVFY
         1 (1 HOWELCHEITH HONHGHVEND ESWHEMBERI YECLDHETEF FAFTLPHYML
                    ....
         .91 APPETEMARS PSEKERHYHE DEDLELPKER NOULTSTACM TAMAVLINGL
         . A DETYMORAÇME RELYMTRYWIN MAWDETYTH HEHGHEDKER WYRSKEWSYL
                                                . . . . . . . . . . . . . . . .
         301 KOGITTADRO YSLENNIHHD IĞTHVIHHLE PQIPÊYELVE ATEAAKEVLG
                                       ==:::::=
         351 EYTERPOESS PLPLHLIGIL AKSIKEDHEV SDEGDVVYYE ADPNLYGEIK
         4.01 YTAE
 HITS AT: 121-125, 157-164, 281-265, 324-328
 ME
       Umspecif.et
 G:
      MAN
 SH
 LC
       STN Files: CA, CAPLUS, TOXLIT
                              KATHLEEN FULLER BT/LIBEARY 308-4230
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1 REFERENCES IN FILE CA (1:67 TO DATE)

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1 REFERENCES IN FILE CAPLUT (1967 TO DATE)
            1: 110:153376
REFERENCE
126 ANSWER 31 OF 36 FEGISTRY COPYRIGHT 1937 ACS
    149955-98-6 REGISTRY
FIL
    Desaturase, fatty and DELTA.15- (Brassida hapus clone pPNSF3-f2
     C-terminal fragment reduced) ( MCI) (CA INDEX NAME)
OTHER NAMES:
    .PELTA.-13 glycerolipid desaturase (Brassica napus clone pENSF3-2
    milorosomal:
    FROTĖII SEĻUEDCE
©Ģ⊑ 378
         1 INTVISSSOPP TEEEPRIGEF DEGAPPPFUL ALIFAAIPKH CWVKNPWKSH
31:0
        51 GYMUFELAIM FALAAGAAYL MUWLYWPLYW LAQGYMFWAL FYLGHDCGEG
       101 GFSMCPELMG VVOHLLEGSI LVEYRGWRIS HETHEOMEGH VENDESWEEM
                                             (100 7 ) 20 20 10 10 20
       151 FERTYKSLOK PTREFRETLE LVHLAYPFYL WARSEGEKGS HYHEDSELFL
       . 01 PKEENEVETA CARMTANAVI INCINEVNAR MÜNIBIAVIR YWINYMWIDE
       .31 UTYLHEHOHE DKWEWYFORE WOYLNGGLTT LIRDYGRIND THEDIĞIEVI
       -Q1 HHIMBQIMBY HIMBATERAK EVILOKYYEEP DENGELELEL IGILAKSIKE
       -51 DEFUCERDU VYVEADENDY CELEVIAE
HITS AT: (5-49, 181-19-, 181-19-, 198-19-2
MF Unipedified
C. _
    M-1
    CT_1
     STM Filed: CA, CAPINE, TOXICE
               1 REFERENCES IN FILE CA (1.67 TO DATE)
               1 REFERENCES IN FILE CAPLUT (1907 TO DATE)
PREFERENCE 1: 11 4:1501 6
IN 6 ANDWER 3. OF 36 EERISTEY COUNTIGHT 1997 ACM
    149955-97-5 REGISTRY
     Departurase, farry and .DELTA.li- (Arabid pair thaliana clone
     pACF2-. i (buch at 171) (CA INDEX NAME)
OTHER NAMES:
    ...ELITA.-1 fatty acid desaturase (Arabidopsis thaliana clone pACF2-2
Ci.
    p. :5ti::)
     .crega.-. fatty act: des durace Arabidopsis thaliana chloroplast
    clare CFI sere fadi precursor
     ..mega.-0-Fatty act: desiturare Arabidop is thalidha clone g45)
     FROTEIN SEQUENCE
F. .
SUL
    446
         1 MANUNUSEDA LAPLARIYET ARMALSIUN KARASISSIS YKISSARISA
SEQ
        51 GLINESGETE NEWLINDSOFT STELLFEESEL EFINEDFEDE GAPPPENLAD
       101 FRAAI PEECW VEUPWESUSY VURIVAIWYA DAGGAAYIND WIVWPLYWDA
       151 OGTHEWALFY LOHDOGE OF SIDERLING V OHILE SILV PYEGWEISHE
                          1=1= ;=
       201 THEQUEGROE NORTWEENCE HITTSTIDET REFERTIELY MLAYPEYIMA
       351 KSPGEEGOHY HEDWOLFLEK ELECVETSTA CWYAMAALDY CLNETIGEIO
       301 MLELYGIPYW IMZHWIDEVT YDHHHGHEDK DEWYE REWS YLEGGLTTLD
                                   = 21= 11=
       351 ROYSLINNIH HOIGTEVIHH LEPPIPHYHL YEATEWAKPY UGKYYKEPDK
       401 SGPLPLHLLE ILAKSIMEDH YUSDEGEVUY YKADPNLYGE UKVRAD
HITS AT: 165-167, 199-206, 323-527, 366-370
                           KATHLEEN FULLER BT/LIBEARY 308-4290
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• MF
    Unspecified
 CI
     MAN
 JP.
     CL
      STN Files: CA, CAPLUS, TCXLIT
                4 PEFERENCES IN FILE CA (1967 TO DATE)
                4 REFERENCES IN FILE CAPLUM (19-7 TO MATE)
 PAREPENCE
             1: 1.1:397 = 33
 FEFERENCE
            2: 110:184023
 SAFEFEN E
           - 3: 1L0:47048
 PEFFENCE
           4: 119:133576
 1.6 AHOWER BE OF THE EMGISTRY COPYRIGHT 1997 ACS
     149955-96-4 FEGISTEN
     Devaturase, :atty arid .DELTA.13- (Arabidopsis thaliana clone pCF3
      resuced) ( *CI) (CA INDEX NAME)
 CTHER NAMES:
     .IMLTA.-15 desaturase (Arabi topsus thaliana clone pCF3)
      .omega.-3 fatty ac.d desaturase (Arabidopsis thaliana clone CF3 gene
      fa\cdot (3)
 \Xi^{\prime}
     PROTEIN SEQUENCE
 SQL 386
         - i Myvaltojeti vnsjegagje ekebredpja oppekigjer aaipkhowyk
 EEQ
         El SPERCMAYUM EDILAWAALA TAAVYVDSWF EWELYWAAQG TEFWAIFVEG
        101 HOGGEGUEDO DECUMENTOSE ILESFILVEY EGMELSEETE HOMEGHVEND
            51000-1
        151 EYWYDLFERU YERLBHSTFM DEYTYPLPHL AYDLYLCYBS PGKEGSHFNP
        . OI YOSLFARSER FILIWISTTOW DINEVSLIAL SEUFGELAVE KVYGVPYLIF
        SET VAMILIANTY, HIHOHIEFIE MYRGKEWSYL EGGLTTIDED YGIFMNIHHD
                       == ==::
        ROLL IGTHULEBLE EQUERYHIND ATKAAKHVLG EYYEEFKTSG AIPIHLVESL
              ==000
        SEL VASIKKEHYV SOTODIVFYE TOPOLYVYAS DESKIN
 HITS AT: 111-165, 137-141, 161-165, 304-308
     Unipediried
 31.
31.
     MAH
     Ci.
     STU Files: CA, CARLUS, TOXICT
. REPERENCES IN FILE CA (1.67 TO DATE)
                . REPERENCES IN FINE CAPLUS (1987 TO DATE)
 SEFERENCE 1: 101:10648
 FEFERENCE 3: 119:11337+
 126 ANIMER 34 OF SO REPLATRY COPYRIGHT 1997 ACE
      148814-49-7 REGISTER
 F. ' J
      Desaturase, :atty and d.DELTA.18- (Brassina napus clone pBNDESS gene
      f.13 reduced OCT (CA INDEX NAME)
 OTHER MAMES:
     . mega.3 L.n. Leate messturase (Arabi lops). requoed)
      PROTEIN SEDUENCE
 FS
 SQL 383
          1 MYVAMBDELIN VNEDSBARKE EGFDPSAOPP FKIGDIEAAI PKHCWVKSPL
 SEQ
         51 RSMSYVTEDI FAVAALAHAA VYFDSWFLWP LYWVAQSTLF WAIFVLGHDC
        101 GHGSEGDIPL LNSTVGHILH SFILVPYH W RIGHRTHHOM HGHVENDESW
                                                 151 VPLPEKLYEN LPHUTEMLEY TVPLFMLAYP IYLWYRSPGK EGSHFNPYSS
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201 LFAPSEPKLI ATSTTCWSIM LATLYYLSFL VDPYTYLKYY GYPYIIFVMW
       261 LDAVTYLEHH GHIEKLPWYF GKEWSYLFGG LUTTEFLYGI FNNIHHDIGT
                   ::== ==
        POI HVIHHLEPÇI PHYHLVLATE AAKHVLGETY KEPKTSGAIR IHLVESLVAS
       -51 INFERRYSET GELVEYETER DLYWYASDES KIN
HITS AT: 98-190', 134-141, 458-262, 301-305
11F
     Unique cified
(T)
     MAH
\Gamma
     C75
     STN Files: CA, CARLUS, TOELLT
1,0
                . FEFERENCES IN FILE CA (1:67 TO DATE)
                .. FEFEFENCES IN FILE CAPLUI (1967 TO DATE)
PEFERENCE
            1: 121:197699
           - H: 119:31:629
FF FEFEINGE
11.6 ANGWER 35 OF 6 FEGISTEY COPYFLIGHT 1997 ACS
    148734-39-8 FEGICTRY
     Besaturace, lineleate (Type thodystas strain PCC 6800 clone csy75-3.5
     reduced 1901. OW INDEM MAME
CTHEF MAMES:
    .DENTA. - 6-Desaturase (Symeon eystis blone pSyl5-3.5)
CH
     Desaturase, limeleate (Cynetheottis strain PCC 6803)
GerBank Powlid-derived protein 01 1605589
Protein Cynethocystis strain PCC 6803 clone
osll23/de0118-pecil4/os0681/rs0094 open reading frame s110262
CT
(11)
     reduced:
     PROTEIN SROUBUCE
L
     359
         1 MATABRIKET GKEGFREVIN JEWINAYFARH GLTQRONPSM YAKTLIIVAW
. . . . .
         31 DEPARAPMER ADVIEDURLE OCTULATADA ARRENOGADA NENAYSSNEH
        1 1 AMENIAMIYA EVELSSELWE VEHNYLHHIY INILGHOVEL HODGAVEMSP
        151 EQERUGIYER QQEYIMGLYL FIREMWELYD VYLVLNKGHY HDHKIPPEQP
       HOLDELANDERE DEWEGYUNGE PEALBESTER VUIGARVIYM TYGIVVCTÎN
       251 MLAHMLHOTE FELIPDORAGA IEDHWAIC, 2 RITANFATNN PHWNWFCGGL
        ROLD NEGOTHELFE HITHIETEQUE ENITEDVOJE FENEYKVYET FKAAIASNYR
       - 0-1 WIEAUGHAS
HITS AT: 88-92, 123-113, 343-394
     Thupedited
7.1
     MEGI
. 1 L.
     CA
     STM File: WA, CALLUS, TOKEAT, USPATFULL
                1 REFERENCES IN FILE MA (1967 TO DATE)
                 4 REFERENCES IN FEDE CAPLUS (1967 TO DATE)
             1: 120:389+6
EEFELENDE
             2: 126:7091:
REFERENCE
             5: 110:154315
REFERENCE
REFERENCE
             4: 110:6401:
ER6 ANSWER 35 OF 36 REVISTRY COPYRIGHT 1997 ACS
     131198-85-1 REGISTRY
101
     Desaturase, anyl coenzyme A [Saccharomyces derevisiae reduced] (9CI)
CN
      (CA INDEX NAME)
     PROTEIN SEQUENCE
                              KATHLEEN FULLER BT, LIBRARY 308-4290
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• SQL 510
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1 MPTSGTTIEL IDDQFPKDDS ASSGIVDEVD DTEANILATG LNKKAPRIVN SEQ 51 GFGCLMGSKE MYSVEFDKKG NEKKSNLDEL LEYDNQEKEE AKTKIHISEQ 101 PWTLNNWHOH LNWLNMVLVC GMPHIGWYFA LEGKVPLHLN VFLFSVFYYA 151 VGGUSITAGY HRIWSERSYS AHWPLRLEYA IFOCASVEGS ARWWGHSHEI 201 HHRYTDTLED PYDAREGLWY SHNGWMLLEP NPFYEAFADI TDMTDEWTIR 251 FQBFHYILLM LLTASVIPTL ICGYFFNDYM GGLIYAGFIR VFV1QQATEC 301 INSMARYIGT OPFODERTER DEWLTAIVER GEGYRNERHE FPTDYRNALK 351 WYQYDPYKVI IYLTSLVGLA YDLKKFSQNA IEFALIÇQEQ KHINKKKAKI 401 NWGFYLTDLP MWDWQTFLAK SKENKGLVII SGIVHDVSGY ISEHFGGETL 451 IKTALGYDAT KAFSGGVYRH SNAAQNVLAD MEUAVIYESH NSAIFMASHE 501 GEIYETCKFF HITS AT: 198-202, 335-339 Unspecified CI I:AM SR STN Files: CA, CAPLUS, TOXLIT LC 1 REFERENCES IN FILE CA (1:67 T: DATE)

1 REFERENCES IN FILE CAPLUS (19.7 TO DATE)

REFERENCE 1: 114:18574